

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAAGGCACCG	CTAGTTTGAA	CCAAACGGAC	ATTCGACCGG	CAACGAAAC	GAAGAACACA	60
ACCATGAAAC	TTCTGAAATC	CATGGGCA	GGCTTAACTT	CGCGCGCTCC	ATTCGGGGCC	120
CGTCGCGGCG	CTCTGACTTC	GTTCATGGCT	GGCGCCCGCG	TCTTATACCA	ATGCGAAGCC	180
GTCTCTTCCG	GGCGGCCACT	GGCGTGGAC	CGCGCATCGG	CGCTTACGGT	CGCGACCGCC	240
GGCGAGTTCG	CGCGCTGCT	CAACAGCTTC	GGCGATCCCA	AGGTGTCGTT	TCCGAACAG	300
GGCGACTTCC	TCAGGGCGG	ATCGGGGGCG	ACCGAGCGCG	GGATGGGGCA	TCAGGAGCTG	360
ACGAGACCGG	CGCGAGCGCG	GGATTTGGCG	CTCTCGTTCA	CGCTGACGAA	CATCGAGCGG	420
GGGGCGCGCG	CTTCGGGCCAC	CGCGTACGTT	TCCTTTCGCG	GTCCGAGCT	CTCGTGGCG	480
GTGAGCGAGA	AGCTCACGTT	CGTCAATCAA	GGCGGCTCGA	TCCTGTCACCG	GGCGATGGCG	540
ATGGACTTCC	TCGAGGGCGC	AGCGAGACTG	ATTCGGGGCG	GGGTTTCAGC	CGCTTCTTCA	600
GCTACCGCGG	CGCGCTGGCG	ACCGCTCCAT	CTCGAACACT	CGCGCGCTTA	GGACGGTGCG	660
GTNTCCCGAG	CGCGCGACCGC	ACCGCGCGCT	GGAAAGCGTC	CTCGAGATAG	CTCGTGCCTC	720
GGCGACCGAG	ANCAACCCCG	ATTCGCGCGT	TCTCGCTGTT	GGATGAA		786

(xii) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCACTAAC	ATCAACATCA	CAATGAGTC	ACGGTACAGA	CGCGCTCGCT	CTTCGGCGCA	60
GACTTCTCA	CGCGACTCGGA	CGCTCTCGCG	CAACCGCTTA	CGCGAGCGCG	CTCTCGCGCG	120
GTGGAAGGG	TCGGCGCGCG	CTCGCGCTTG	CTCGTACTCA	ACCGAGCGCG	CAACGGCGCG	180
TCGGCGCTTG	TCATCGACCA	ACCGCTACG	TCGGCGCTTC	GGCGATCCGA	CGCGGACGTA	240

TTTCTCGAAG ACCCTGACGCT GACCCGTCGCG CAGCTGAAAT TCCGGTTGGA AAACAAUAA	300
TTCAATGTCG TCGCTTCTCG GACTCTTACG CGCGCTTACG TCAACCGCGA CGCGCTGAT	360
TGGGGGGTGC TGGCGAACGG CGACGAGCTC CAGATCGCGA AGCTCGGTT GGTGTTCTTG	420
ACCGGACCCA ACCGAGGCGA CGATGACGCG AGTAACGGCG CGCGCTGAGC CGACCGUGTA	480
CGCGCGCGT CGCGCGATG TCCATCGCGG CGCTCGTCGG ACCTGCTACG ACCGGATTT	540
CGCTGATGTC CACCGATCTCC AACATTCGAT TUTTGCGAG CGTTCAGCTC CGCGTGACCG	600
CGCGCGCGCG CGTATTCGGC GGTTCACCC CGTACGACT CGCGCGCGCG	660
TTCGAATTG TTTCGTCAGT CGCGCGCG CGCGCGCG CGTACGACT CGCGCGCG	720
CGCGGGCGG TTGCGTGAAG CGCGCGCG CGTACGACT CG	780

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
CTATATCCATC ACCATCAGCA TCACACTTCT AACCGCGCGA CGCGCGCGCG CGCGCGACGA	60
CGACCGACG CGCGCGCGCG TCCATCTCGT AGCTTGACTC TGGTCACCGA TCGCTCGTCG	120
CGCGCGCGT CGCTATGTTT GTCTCGACT CGATATCGG CGCGCGCGA TCTCGCGCGT	180
GGCGCGCGCG GTGCTGCAAAG CTACTCGCG AGAAATTTCG AGCTCGCGAT CGAGATCTTC	240
ATCTCTGGCA CGCGCTGCTG TTTGCTCTGT TGTTCGGGTC CGCGCGCGCG CGCGCGCGCG	300
ACCTACTGCG AGGAGTTGAA AGCCACCGAT ACCCGCGCG CGCGCGCGAT TCAATGTCG	360
CGCGCGCGCG ACACACGCA CATCGCGCTG CGCGCTTACT CGCGCGCGA CGAGATCGCG	420
CGAAATTACA TCGCGCGACG CGCGCGCGCG TGTCTCGCG CGCGCGCGAT GTGCGACTCGA	480
CGCGCGCGCG CGTACGACTT GAATATCGCA CGCGCGCGAT ACCAGTCGG CGTACGCGCG	540
CGTCTGACCG AGGCGCTGCTG CGTACGACTT TCTCGACCG CGCGCGCGCG CGACCGACG	600
ACCGACGCTCA AGCGCTTGAAG TTGGGGACCG CGCGCGCGA AGCCACGTCG CTATCGACCG	660
CTTGTGCGACG CGTACGACTA CGCGCGCGCG CGTCTGCGA CGTACGACTT AGCGTACGACT	720

GACCAAGGCA GACCCGCGCA ACAGGTTATCG ATAGGCGGCGT AATGCGCGCT TGGAAACCGCG	786
TGAAATTATC ACAAACTTCGGC AGTCACAGAA NNN	813

(2) INFORMATION FOR SEQ ID NO:4:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCTTATGAAAC CGGGCGCGCTT CGGATAACTT CGCGCTGTCG CAGGGTGGGC AGCGATTCCG	60
CATTCGGATC CGGGCGCGCA TCGCGATCGC CGCGCGATC CGATCGCGTC CGGGGCTCAGC	120
CGCGGTTGAT ATCGGGGCTA CGCGCGTCTT CGCGGTTGGGT GTTGTGCGCA ACAACGGCAA	180
CGGGCGCGA GTGCGACCGC TGGTGGGAG CGCTCCGGCG CGAAGCTCTCG CGATCTCCAC	240
CGGGCGCGTG ATCGGGCGCG TCGACGGCGC TCCGATCGAC TCGGGCACCG CGATGGCGGA	300
CGGGCGTTCAC CGGGATCGTC CGCGGTGACG CTGCGCGTC AACTGGCAA ACGAAGTCGGC	360
CGGGCACCGT ACAGGGCAAC TGAATTCGGC CGAGGACAC CGGGCGCTAT TTGGTGGYGG	420
ATACCGACGG CGGGCGCGCG AATTGGA	447

(2) INFORMATION FOR SEQ ID NO:5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCGCTCG CGTGGCGCGAG TATGTCGCGCC AGCAATGTC TGGCAGCGCG CGAAGGAAAT	60
CGCGGTGATCC GACGTGGCGAG GTTGTGAAAC CGGGCGCGCG CGAAGTATCG CTGGATCGCT	120
AGGGCGCGA CGGGCGCGCG CGGGATCGCG CGAAGTGAAGA CGGGCGCGAT TTGGGGGGGC	180

CCCGCGACGG	CGACCGCGCG	AACTGGCGCGAA	GTGAGGAGGT	GCGGAGCTAT	GGCGCGAGCTG	240
ATCCGAAATCAA	CCTGCGATTCG	CGCTGCGCGAA	CGATTTGACA	ATCCGAGGTAC	TGCGCGCGAA	300
TGCGCGATCG	AAAGACCGCG	GGCGACCGCG	ATGCTTCTGCG	CCTGCGATCG	CGCTGCGCG	360
ATGCGCGGCT	ATCAGGCGT	TCTTGCAGCA	AAACCTGATCG	CGACGGACAG	GCTGCTTCCCG	420
CGACCGCGAA	CGCTGCGCG	TGCGCGATCG	CGACGGACAG	ATGCGCGGCT	CGCTGCGCG	480
AAAGACCGCG	CGACGGACAG	ATGCGCGGCT	CGCTGCGCG	AAAGACCGCG	CGACGGACAG	540
AAAGACCGCG	CGCTGCGCG	AAAGACCGCG	CGACGGACAG	ATGCGCGGCT	CGCTGCGCG	600
AAAGACCGCG	CGCTGCGCG	AAAGACCGCG	CGACGGACAG	ATGCGCGGCT	CGCTGCGCG	660

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCGCGANGTCG	AACCCGCTCA	CTAAAGCGAA	CGAAGGCTTG	AGCTCGACCG	CGGTGGCCCG	66
CGCTCTAGAA	CTAGCTGATG	TTTCGCGCTG	CGAGGATCG	GTACCGCTAT	TAGGACGCTC	120
TAACCGCTCT	CTTACCGCTGA	TGCAATCGCC	GAAGACATCC	TGCTGATCGA	CGACCGACAA	180
CGCGTCCGAA	CGCTCACCT	CAACCGCGCG	CGATCCCGYA	ACCGCCCTTC	CGCGCGCGTA	240
CGATCGCTG	TTTTGGCGGT	GTGCGGCGCG	GGCGAGGCG	ACGACGCGAT	CGACCTCTTC	300
ATCGTCACCG	GTGCGGCGCG	GGTGTTCGCG	GCCTGACTGG	ACCTGACGAT	AGCTGGCGCG	360
CGAGACCGCG	CTGCGCGCGA	TCTCACCGCG	GTGGGCGCGCG	ATGACCGACG	CGCTGATCGG	420
CGCGATCGAC	CGCGCGCGCG	CTGCGCGCGA	CGCTGACTGG	ACGCTGACTG	CGCGCGCGTA	480
CGTCCGCGTC	CGACCGCGCG	GTGCGGCGCG	CGACCGACGCG	CGCTGCGCGCG	TGCTGGCCCG	540
CTGCGCGACTC	ATGCGCGGCT	TGCGCGCGAA	GTGCGGCGTC	CGCTGCGCGCG	CGTCCGCGTC	600
CGTCCGCGCG	CGTCCGCGTC	CGTCCGCGTC	CGTCCGCGTC	CGTCCGCGTC	CGTCCGCGTC	663

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGACGCCACG GTCACCCGGG GTCACCCCTGC GCGGCCGAGG AA	1362
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(2) INFORMATION FOR SEQ ID NO:8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGACGCCACG GTCACCCGGG GTCACCCCTGC GCGGCCGAGG AA	60
CTATTCATTC CGTTTACGGC ATTCAAGACT GCTTGAGGCC CGCTCTGGGG GAAACCGTGC	120
TGCACTGACT CGCCCGCTTT TACATCATCTT ATCCGGACCG GCGGCCGAGG CTGGCGACCG	180
CTTAAGGCGTT GCTCGCGCTG CGCGACGACT TAAAGCTGAG CTTCGGCGGC GTCACCGTAC	240
TGCGCGACCG CTATCTTCG CACCAAGACG AGCGCGCGCC CGCTCTGGCG AGCGCGCGCG	300
TCATCGACCG ATCGCGCGAC TGTGTCCCG CGCGCGACCA CGCTCTGGCG CGCGCGCTCG	360
CGACCGCTG CGCCGAGGTT TTOGCCCGCC TATTACCGAA CGCTGATTC CGCGCGAATT	420
CGCCGAGTT CGTGAACCTT GGCACCGACG TGGACTGCT CGCCGCGCTGT TTTGTTCTGC	480
CGATTCAGGA TTGCGCTGAA TCGATCTTGC CGACGCTGCG ACAGCGCGCC GAGCTCGACG	540
CGCTTGCAGG CGCCGACCGA TATCGCTGCA CGACGCTGCG ACCGGCGCCG GATCGGGTGC	600
CGTCACCGCC CGCGCGCGCC AGCGCGCGCG TGTCTTTCTG AGCTCTGTAT CGACGTCGG	660
CGCTGTGCTG CTCCATGCGC CGTCCCGCGCC GTCGGCGCTG TATGGCTGTC CTTGATGTGT	720
CGACACCGGA TATCTGTAT TTGCGCTGCG CGAGGGCGGA ATCGCGCGAC GAGCTCGCC	780
ATTCGAACCT ATCGCTTGTGT GTGACCGACG CGTCTCTGCG CGCGCTGAA CGCAACCGCC	840
TACGCGCGCT CGTCAATCGCG CGAACCGGGCA AGATCGCTGC CGCTGATTC CGCGCGCGAC	900
TGTTTGACCG CAGCTCGAA CGCGCGCGCG CGGTGGCGCA TCGCGCGCTG GTTCTTCTGC	960
ACGCGATCAA TACGGCGACG CGCGCGCGCG CGAGGGCGCG CGTCAACCG ACCGACGCT	1020
CGCGGGACGT CGCGCGCTGC CGTACGCTGT CGTCAATCGCG CGCTGATTC CGCGCGCGAC	1080
CGATGCTGCG CGACCGCTGC CGTCACTGCG ACCGGCGCGA AGAGCTCGACG CGTGTGGCGC	1140
CGCGCTTGTGT CGTCAACCGT ATCGATGTCA AGCGCTGCG CGTCAACCGA CGCGCGCGAC	1200

CGGGCGCGCG	GGACCCGCGAG	ATCGCGCTCG	CGTCGATCG	TTTGGCGCGAA	CTGCGTCCCG	1260
CACTCGGCGAT	TCCCTACCGAC	AGTGAAGAAG	CGCTCGGCGT	AGCCACCGCG	CTCAGTCGTC	1310
GGCATCGCGCA	GGCCCGCGCG	ACCGATCGCC	GGACCGCGCG	GGAGAGCGCG	GGCGCGATCG	1380
CGCGCTTCAC	CGTATCGCCG	TTGCGCGGCT	CGGGCGCGAG	GGCCACCGCG	CGGGTCACCT	1440
CGCGTCGCGAC	CGACCGCGCG					1450

(2) INFORMATION FOR SEQ ID NO:9:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCTGTAAT	CCTGCTGCGAT	CTGGAAACCCG	CTGGCGCGCT	ACCTTACCGAG	ATCTACTGGC	60
GGGGTACCGG	CGTGGCCGCTG	GGCATCGCCG	TCTGCGTACG	CGGGATCGCG	CTGGCCGATCG	120
TCTATCGCGTT	CCTCGACCGAC	AGGCGCGCTG	CGGACCGCT	CGGGCGCGAC	ANGCGCGCTT	180
CGGGCGCGAG	CGATCGCGAC	TGGCGCGAC	CGGAGCGCC	CGACCGCGCG	GGCGAAACCG	240
AAAGTAAACG	CGGCGCGCGC	CGGGCGCGG	CGGAGACCG	CGAGAGACCG	AGGGCGACCG	300
CGGGCGTCAA	CGGGCGCGCG	CTGCTCAGG	AAAGGCGCGA	TTGGCGCGAT	TGAGCGCTCG	360
CGCTCAAAAG	TTTGACCAAC	CGGCGCGACT	ACTACGTCG	CGACCGCGCC	AAAGTCACCA	420
TGGTGGTCA	CGACATCGAC	CTGGCTGCGT	CTTAACCGCA	CGTGGCGCG	CGGGTGTGG	480
CGGGCGTACG	TTACTCGCTG	CGACACCGAC	CGTTGCGCTG	CAACCTGGAC	TGGCGCGCTT	540
CGATGCGAC	CTGTGTCAG	ACGTTTCCG	CGTGGCGCA	CGTACCGAC	CGGGTGTGG	600
CGACCGCGAT	GGCATCGCG	CGGGCGCGCG	CGTGGCGCG	CGGGCGCGAC	GGGGCGCGCG	660
CGTACCGAT	CGTGGCGAC	CTGGCGATC	CGGGCGCGCT	GGGGCGCGCG	TTGAGCGCTG	720
ATCGAGCGCC	GGGGCGCGCG	GGGGCGATAC	CGGGCGCGCG	CGGAGCGCG	CGGGCGCGCG	780
CGGGCGTACG	GGGGCGCGAC	GGTAAATTAT	CGTGGCGAC	TTGAGCGATC	GGGGCGCGCG	840
CGACAGCGCT	GGGGCGCGCG					862

(2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATGAGCA	CCCCGAGGC	GTGACATGCC	TCCCTGGGTC	TCCAGGTCAC	CAATGACAAA	60
GACACCGGCG	GGGCGAGAT	CTGCGAGTA	GTGGCGCGTC	GTCTGGCGC	GAACCGCTGG	120
GTGGCGAGG	GGCTGCTTGT	CAACGAGCTC	GGGAAAGGCC	GTGCGACAG	GGGGAGGCG	180
TTGTTTGGCG	CCCTCGGTC	CAAGCGCGG	GGGGCGAGG	TGTTGCTAAC	CTTTTGGGAT	240
CGCTGGGCG	GTAGCGGCG	AGTCGCGTC	ACCTCGGGCA	AGCGCGAGCA	GTGATGAGCG	300
TGCGCGGCG	GTGTTGAGTC	GTGCGATTC	CGCTGGGAC	CGTGGACAG	CGTGGCGAGT	360
TGCTGCTTGT	GGGGCGACTT	GTGCTGCTCG	TTCACGATCG	CGGGCGGAC	GGCGATGAGC	420
ACCCACGGCG	GGGGCTTTC	ACCGCGCTTC	TCACGACCC	CGTTTTTTC	GTGAGCGCG	480
TCGTTGGCGT	GTGGCGGAGC	GGGTCGAGCA	TCCGAATGCG	CGTGACACCA	GGCGCTGATCG	540
GGGGGGGCGA	GGTGGTGGTC	TGGGTCGCGG	GGGCGGCGGT	GGGCGCTGCG	GAAGTCGACCG	600
CGGAGGCGAC	CCCGACGATT	CT				622

(2) INFORMATION FOR SEQ ID NO:11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGAGCG	TGAGCGTTT	GGGGCGCGGC	AGACTGGGT	TGACGACATG	GGGGCGGGAG	60
ACCAACAGCT	CGTCGTCAGG	GGGAGGCGGA	ACGTCTGGCT	CGCTGCGCTG	GGGGCGCGAG	120
AGCGCGCTCG	AGTCGCGCGC	CTGCGGCGCA	CGGGCGGCGA	CGGGCGGCGC	CGGGCGGCGC	180

GGCTTACGTCG	CATCCTGCCC	GGGGCTCAGC	TTCGACTAAG	ACGCCAAGCG	GTGCGGGTCCC	243
GGGGTGCACCC	ACTTTTCTCAA	CAACGAAAGTC	CATTTCGCGG	GGTGGGATGT	CGGGTTTAAAT	300
CCCTTCACCG	GTGAACTGA	CCGGCTGGCG	GGCGGCTGG	TTTCCCCGGC	ATGGGACCTC	360
CCGACGGTGT	TGGGGCGAT	CCGGTCACCC	TACAATATCA	ACGGGCTGAG	CAACGTTAAT	420
CTTGACGGAC	GUACTACCGG	CAASATTTTC	AAACGGACAC	TCACCGTGTG	CAATGATCCA	480
CAGATCCAGG	CCCTCAACTC	GGGGACGGAC	CTGGGGCCAA	CGGGATTTG	CGTTATCTTC	540
CGGACGGACA	ACTGGGTTAC	GGGGGAAAC	TTCCGAGAAT	ACGTCACG	TGTATGAAAC	600
GGGGGTTGG	CGAAAGGGCG	CGGGGAAAC	TTCAACCGGG	GGTGGGGGT	CGGGGGGAGC	660
GGGAAACGAG	GAAGCTGGCG	CGTACTGCG	ACGACCGCG	GGTGGATCAG	CTACGACGAG	720
TGCTCGTTG	CGATGGCTAA	CGAATTGAC	ATGGGGCGAA	TGTGACGTC	GGGGGGTCCC	780
CATGACACTG	CGATGACAC	CGATGACATC	GGTAAAGACAA	TCGGGGGGGC	CAAGATCATA	840
GGACGAGGCA	ACGACCTGGT	ATTGGACACG	TCGGTGTGTT	ACAGGACCCAC	CGAGGCTGGC	900
TCTTACCCCG	TGGTGTGCG	GGGTTTGGAG	ATGCTGTGTT	CGAAATACCC	GGTGGGAGCG	960
ACGGGTTACTG	CGTTTATGAA	CCCGGGGATTG	GTGCGGGCGA	ACGAGGCGCTG	ACGAGGCGAT	1020
GGCCGATACG	GTGCGATTCC	GGTGGGGCGAA	TGTTTGGAG	CAAAATTGGC	GGGGGGGGTG	1080
AATGCTTATTT	CTTGACCTAG	TCGGGGGAT	TCGACCGTGA	GGGATGGCGT	TGCGGAGGTA	1140
GGGTGGGCGAT	TTGGGGCGTA	TCGGGTTATTG	GGGCTGGTGC	GGGGGGGCG	GTGGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGAGGCGGT	CGAGGCTGTG	CTGGTGGACCG	AACTGGGCGAT	GGGGAAAGGCC	AAACGGACCGA	60
AGACCGGCGTA	CGACGCGGAT	GGGGAGGGCG	TGCACTGTT	GGTGGACACAG	ACCGGGCGATC	120
CGTTTGTGCA	ACGATGCGTC	GGGGGGGGCG	ACGTCACGCG	GGTGGGGCGTC	ACCGGGCGACG	180

GGTTCTCTCA AGCCGTTGGC CGGACGGCC CGATCAGAC CACGTTAAC CAGACGATCG	240
CGCCGACCGC CGCGCTCTCC TGGACGAGC CGAACCTTCA GAACATCCCG ATCGCCGACCG	280
ACCGCGCGCG CGCGATCGCG CGCGGTTCC TGGCGGCG CGGTTACGGC GAGTTGATCG	320
CGCCGCGACTA CAGCGACATC GAGATCGGGA TCGATGGCGA CCTGTCGGCG GAGGAGGCGC	360
TCATCGAGAC CTTCAACACCC CGGAGGAGCC TGTATTTGTT CGTGGCGCTC CGGTGTTCC	400
GTGTCGGCAT CGACGAGCTC ACCGGCGACT TCGCGCGCG CGTCAGGCGCG ATGTCCTACG	440
CGCTGTTTA CGGTTGAGC GAGTACGGCG TGGCGGCGA GTTGAAGATC TCGACCGAGC	480
AAGCCGACGA CGAGATCGCG CGTATTTCG CGCGATTCCG CGCGCTGCCG GAGTACGCTCG	520
CGCGCTTACT CGAGCGGGCG CGAGAGGAGC GAGACGCGTC GAGGTTGTCG CGCGCTGCCG	560
CGCTACCGCG CGACGTCGAC AGGAGCGACCG CGTAACTTCG CGAGGCGCGCG GAGCGGGCG	600
CGCTGAGCG CGCGATCGCG CGCGCGCGCG CGCGATCGAT CGAGCTGCCG ATGATCGAGC	640
TGGACGAGCG CGTCAGACCG CGACGCTCG CGTCCGGCAT CGTCTCTCG CGTCAGCGAGC	680
AGCTTCTTCTT CGGATCGCG CGCGCTTACT CGAGCTGCCG CGAGCGCGCGA GAGCGGGCG	720
AGATGGCGCG CGCTTACCG CGCGACGCTCG CGCTGGAGT CGCGCTGCCG TACGGCGCGA	760
CGTGGAGCG CGCGCGCGCG CGAGTGCGGA CGTGGCGAT CGGGCGCGAA TTGGCGCGATT	800
TTTCCGGCGT GAGTCACCG CGTGGCGAT CGGGCGCGAG TTTGTCACCG GTGTCACCGT	840
CGAGTACCGT CGTC	880

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAGCGCGCTC TGGTGTGTTGA AGCGTTTAC CGTGGCGCAT CGCGACGACG CGTGGCGGGCT	60
TGGCGCGCTCG CGTGGCGCAT CGTCAGACCG CGTGGCGCTCA ACCGGCGCGCG ATGGTGGCGC	120
ATGAGACGACG CGCGCGCGCG CGGCGAGCG CGCGACGACT CGATTACGCT CGTGCGCGCG	180

GGCGCTGGA	TCGCCGTTCC	GCAGCTTCCC	GTCGCGACCG	CTGGCGCTCG	GACGACGGAC	240
ATCGAGRACT	CTCGGGGTTG	CGCGAACGTT	ATCTGAGTGC	AACTCTGAGTC	CGCGGCGGCA	300
ACCTAATTGT	CGAATTACTG	TTGAAACCCA	CAACCGATCCC	ACTCGACCGA	TGCCCAAGTT	360
GGCCGCGATA	CTGGCGCTAG	TACCGGAGA	GCACGCTACC	GACGTGACGA	ATCGACCCACG	420
CTATTCGCGA	CCGGCGCGAC	AGCCGGGAGC	CGCGGTTAT	GTCGCGGCGC	AGCGCGAAC	480
CTACGGCG	CACTTGACT	GGCGTTACCC	ACGCTCCCG	CCCGCGCGAC	CAACCGATA	540
CCCTGACCC	TACCGGCGT	TGGGTGGTAC	CCGGCGCGGT	CTGATGCTG	GGCTGATTG	600
GGCGTACG	CCCGCTCTG	GGATGGTTCG	CCACGCGCGT	CTGCGACCGA	TGTTCGCGAT	660
CGCGCGATA	ACGATGGGG	TGCTGCGCC	CCGGATGCCG	GGCGGGCGG	CATCCGTT	720
CGGGTCAAC	CGGGCGACG	CCGGGCGCG	CGGGCGCGCA	CTGGCTGCCA	GGGGGGCGCG	780
AGCGATCCC	CCGGCGACG	TGCGGCGCG	CTGGCTGCCA	CTGGCTGCCA	GGGGGGCGCG	840
GGCGAGTTC	CTGATGTTGG	AAACCGATCT	GGCGCGCGAC	TGCGGCGCG	GGCGCGCGAT	900
CGTTCTGT	GGCGGCGCG	TGATGTTGAC	CAACGCGAC	CTGGCTGCCA	GGGGGGCGCG	960
GGCTTCCCG	GGCGCTGCG	CGCGCGAC	GACGGTAACC	TTCTCTGAGC	GGCGGCGCG	1020
ACCGTTACG	CTGATGTTGG	CTGCGCGAC	CTGGATATC	GGCGGCGCG	CTGTTGAGG	1080
CTTCTCGGG	CTGACCGCGA	TCTCCCTGG	TTCTCTGCG	GGCGGCGCG	TGGCTGAGG	1140
GGTGCTGGG	ATCGCGCTGC	GGCTCGTTT	GGACGGCGCG	CTGACGACCG	GGATGGTCAG	1200
CGCTCTGAC	CGTGCCTGT	CGACGCGCG	CGAGGGCGCG	ACGCGACGCA	CGCTGCTGCA	1260
CGCGATTCAG	ACGCGACGCG	GGATGACCGC	CGTAACTCC	CGCGGCGCG	GGCGGCGCG	1320
GAACGCTCAA	CTGCTGGGAG	TCAACTGCC	CTGGCGCG	ACTCGACCGA	GGGGGGCGCG	1380
TGCGCAGGCC	GGCTCGATCG	GTCTGCTTT	TGGGATCCG	CTGGCGCG	GGAGGGCGAT	1440
CGCGCGCG	TTGATGAGCA	CGCGCGCGC	CTGACGACCG	TGCGGCTGTC	GGCGGCGCG	1500
CAATGACAAA	GGACGGCGCG	CGCGGCGCG	CTGCGACGTA	CTGGCGCG	CTGCTGCGCG	1560
GAACGCTGGA	CTGCGCGCG	CGCTCGTTG	CGACGAGCTC	GAACGCGCG	CTGCGACGCG	1620
CGCGCGCG	TTGCTTGGCG	CGATGCGCTC	CAAGCGCG	GGCGGCGCG	TGGCGCTAAC	1680
CTTTCAGCT	GGCTCGGGG	CTGCGCGCG	ACTCGACCGC	AACTCGCGCA	AGCGGCGCG	1740
CTGATGACCG	TCGCGCGCG	CTGCTGAGG	CTGGCGCG	TCGCGCGCG	C	1771

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCCCG	CTGGGGCG	CTCTAGAACT	AGTGGATCCC	CGGGCTGCA	GGAAATTGGG	60
ACGAGGATCC	GACGTCGAG	TTTCGCGAC	CGGGGGCGCC	CGAACTATCG	CTCCATGGCT	120
ACCCGGCGA	ACGGACGCGC	CGGATGCGC	CGAATGAGGA	GGGGCGCAT	TTGGGGGGGC	180
CGGGCGACG	CGAGCGCGG	ATGCGCGCA	CTGAGGACCC	GGGGCTCAT	GGCCAGCGTG	240
ATCCAACTCA	CTGCGATTCC	GGCTGCGGGC	CCATTTCAGCA	ATCGAGCTAC	TCAGCCCAA	300
TGAATCAGTG	AAAACGGGCG	GTGACGTCGG	CTGTTCTGCT	GGTGTAGGT	GGTTCCTGG	360
CGTTTGGCT	ATCAGGATGT	TTTGGCGCA	AACTGATGCG	CGAGGAGCG	GGTGTGCGG	420
TCAGCCCGAC	GGCGTCGAGC	CGCGCGCTCG	TCCCGAGCT	CAGGCACTCG	CTTGATGCGA	480
CAAAAGCTT	GAACGAGCGT	CGCTTACCG	TCGGACACAC	CGGGAAACTC	GGACGCTTGC	540
TGGCTATTAC	CAAGTGGCGT	CTGGACGCTC	CGGGCGATTC	GGTGGGGCGA	AAAGGGCTAT	600
CGACCTACAA	CGGGAGCGAG	GGTGTGCGGT	TTGGGGGTACA	AGGGAGCGAC	ATCTCGGCTGA	660
AACTGTTCAA	CGACTCGAGC	TTTGTGGCT	CGATTTCGTA	ACTGTGAACT	TCAGCGGTGC	720
TCGATCTCC	CGCTGGGGTC	ACGCGCTGC	TGTCCGCTAT	CAAGAACCTC	CAASCCGAG	780
GTACCGAACT	GGTACGACCG	ATTTGACCA	CGAACATCAC	GGGGCGATCG	CGCGCGACGT	840
CTGTCGAGAT	GGTTGATCCT	GGGGCGAGA	CTGCAAGGCG	GGCGACGCGT	GGTATTGGCC	900
AGGACGGCTC	CGACCGACGTC	GGGGAGCGA	GGTCAAGGCG	GGGATCGCG	TCGATTCAGC	960
TCACCGCGTC	GAATGGCGAC	GAACCGTCA	ACGTGCACTA	GGGGAGCTT	GGTGGACGCC	1020
CTTGTGCGA	ACGGCCTTTC	GAAGGGTGTG	ACGCGACAC			1088

(2) INFORMATION FOR SEQ ID NO:15:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAATTCCGCA CGAGAGGTTGA TGCACATCAT CGGACCCAGC CGCACATCCY GGGACACAGCC	60
CGGGGGGGAG CGGCTCCAGC CGGGGGGGGA TACCTCTCAT GACATCCGGG CGGCTCGGTT	120
CTTTCACCCG GACATGGGCG TGGACAGGCC CGGGAGAGTC ACCTACCCGA TCAAGCTCGA	180
AGCTTCTTTC AAGATGAGGC CGGCGCAACC CGCTTACGAC CGGGGGGGGA CGAGAGCGCA	240
AAATCCGAGG GTTTCGCGT GATTCGCGG ATTTTGTGTC TCTCTCGGA CGCTTACCGAG	300
GGGGGGGGAA CGTCCCGCTG CTGGCGTATC GACCGCTCGA TCGCTATTCC CGGGGGCGCG	360
CGGGCTTAA TCGTTCCCGT CGCGCGAAC TGGCCCTTCG CGGGGGAGTC TATCGATGA	420
CGCTGGGGAG CGCGCTCGATG CGCGATTGCG CGGAGGAAAC CGCTTACCGAG CGCGCTCGAG	480
AGCGTTCGTA CGCGCGGATG CGACCGCGT CTGGCTCGTC CGCGCTTAA CGCGCGCGCC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGTGGCGCC CGGGGGCTCGG TTGCCCCCAT TGGCGCTGTC CGCGATCAGC TCCGCATCGC	60
CACCATCGAC CGCTTCCCG CGGGGGGGGG CGCTGGGGCG CGGGGGGGGG ATGGCACACGG	120
TTCGCGCTGG CGGGGGGGGG CGCGATTGCG ATAGCGAACG CGGGGGGGGG CGCGTTACG	180
CGGGGGGGAA CGGGGGGGGG CGCTGGCGTT TCGGGGGGGG CGGGGGGATG CGACCGCGCG	240
CGAGCTGGGG CGGGGGGGGG TTGGGGGGTT TTGGGGGGGG CGGGGGGGGG CGCGGAATTG	300
CGGGGGGGAA AGCGCGCGTT CGGGGGGGGG CGGGGGGGGG TAACCGCGGT CGGGGGGGGG	360
CGGGGGGGAC CGGGGGGGAC CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	420

GTTCGCGCTT AATATTCGGC GGGACCGCC AGACCGCGC GGGCCACCT TGGCGCCGCG	480
CGCGGAAAGA ACAGCGGAAAC GGTGGCGCGG CGCGGCGCTT TTGGCGCCGAT CGCGGCGCT	540
TGGCGCGCG CGCGGCGCTT AATGTTTATG AGCGCGCTG CGCGCGCGG CGCGCTATTG	600
CGCGCGCGCG CGGNGCGCTG CGCGCGCGCG CGCGCGCGCG CGAAACCGCG CGGTTGCCAC	660
CGCGCGCGCG CGACCGACCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	720
TGGCTGCTGT CGACCCGTTA CGCGCGCTTC CGCGCGCTTC CGCGCGCGCG CGCGCGCGCG	780
CGCGCGCGCG CGTGGCGTAC AGCGACCGCG CGCGCGCGCG CGTGGCGCG CGCGCGCGCG	840
TGGCGCGCGT CGCGCGCTTG CGCGCGCGACG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	900
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACCTTC GTCTTCAAAA ATCTGCGCG CGCGACCGTT AAGGCTTGGG CAAATTCTGA	60
TTGGCTTGGCC CGCACAGGAG GTTACGGCGAT CGACGATTTG CGCGCGCGCT CACTCGCG	120
GTGCTGCTTC CGCGCGCTTC TGGCTGCCG CGCGCTGGC CGCGCGCGCG CGCGCGCGCG	180
CGCGCGCGCG CGCGCGCTAT CGCGCGCGCG CGTGGCGCG CGCGCGCGCG CGCGCGCGCG	240
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	300
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	360
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	420
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	480
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	540
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	600
CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	660

GACATTTAAC	GGGTTGATCC	ATTTGATTC	CCGATTCGAG	CCCGATTTATT	GGGGCGGGCC	720
CGTGTGAAAC	GGCTTACGAC	AGGTGGTCCG	TATGACACG	GGCGGCGGCG	ATAAGCTTCA	780
GCTGTGCGAC	GTGAGGCGGC	GATTCGGCAT	TCGGATCGG	CGCGATTC	CGATCGCGCG	840
CCAAATTCGA	TGGGTTGGCG	GTGACCCAC	GGTTGATATC	GGGGCTACCG	CCTTCCCTCG	900
CTTGGGTTT	GTCGACACCA	ACCGAACCGG	GGCGAGATC	CAAGCTTGG	TGGAAAGCG	960
TCGGGCGGCA	ACTCTCCGTA	TCTTACACCGG	GGACGTGATC	ACCGGGGTCG	ACGGCGCTCG	1020
CATCAACTCG	GGCACCGGCA	TGGGGACCGC	GGTAAACGGG	CTTCATCGCG	CTGACGCTCG	1080
CTCGATGAAAC	TGGCAAAACCA	AGTGGGGCGG	CGCGATTA	GGGAGCTGA	CATTGGCGCA	1140
GGCGCGCG	GGTGGATTTC	TGGCGATAC	CGGGCGCG	CGGGCGGATT	GGATTCGGCG	1200
CGCGCGAT	TCCCGCTGAA	GGGGCGGAT	TCGTTTTC	CTGGCGCTTG	CATTGCGGAA	1260
CCGATTCGAC	ACCCGAGGCA	CGCCGTTG	CGGGTCCCG	TTACGCTCGA	1320	
GGCGCTTGG	TGAGGATTTC	GGATCGGAG	CGCTGGCGA	GGGGGGGGCG	CTCTCCCGCG	1380
GATCGGACT	GTTTAAGCA	GGCGCTTTC	TACGAGGTC	TGTTTTCGGG	GTGTTTCGAC	1440
CCCACCGCG	ACGGTTCGG	GGATCTCGT	GGCTCTCG	ATCGGCTTGA	CTACCTGGAC	1500
TGGCTTGGCA	TGGACTCGAT	GTGTTGCCCG	GGTTCTTACG	ACTCACCGCT	GGCGGAGCGC	1560
GTTTGGACA	TTCGGGACTT	CTACGAGGTG	CTGGCGACGT	GGACGATTTC	CTGCGCTCGG	1620
CTGCGCTCGG	TGACGCGCG	TCACCGCGA	GGTATCGCA	TCTTCAGGA	CTGGGTGATG	1680
ATTCACGCT	CGCGATCGCA	CGCTTGGTTT	CGGGCTCGC	GGGGCGCGCG	AGACGGACCC	1740
TACCGTACT	ATTACGCTTG	GGCGACGCG	ACGGACGCT	ACACGGACCC	CGGGATCGTC	1800
TTGCTGCGACA	CGGAGACGTC	GAAGTGGTCA	TTCGATCTTG	TCGCGGCGCA	GTGTTACTTG	1860
GCACCGGATC	TT					1872

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGGGAA	ACCTGATGCC	GGGGACAGG	GTGTTCCCGT	GGGGGGGCCG	GGTGGGACCC	60
CGCGCGCTCT	CGCCGAGATC	ACCGCGTCGC	TTGATGCCAC	AAAAGGTTTG	ACCGCGCTGC	120
ACGTTAGCTT	CGGACACCC	GGGAAAGTGG	ACAGCTTCT	GGGTATTACG	AGTCGAGATG	180
TGACGCTCG	GGGCAATCCG	CTCGGGGAA	AGGGCGTATG	CACCTACAC	GACGGAGCAGG	240
GTGTCGCCGT	TGGGGTACAA	GGGGACAGA	TGTGGTCAA	ACGTTGCC	GACTGGACCA	300
ATCTCGGCCG	GATTTCTGAA	CTGTCACCTT	CACCGCTGT	CGATCGGCC	GCTGGGCTGA	360
CGCACCTGCT	GTCGGGTGTC	ACGAAACCTCC	AGGGCGAAGG	TACGGAGTG	ATGAGACGGAA	420
TTTCCACAC	CGAAATCACC	GGGACGATCC	CGGCGACCTC	TGTCAAGATG	CTTGATCCTG	480
GGGCGAAGAG	TGCAAGGGCCG	GGGCGCTGT	GGATTCGCGA	GGACCGCTCG	CGACCGCTCG	540
TCCGAGGGAG	CATGACCTTC	GGATCCCGT	CGATTCAGCT	GGGGCACTCG	AAATGGAAACG	600
AAACCGCTAA	CTCGACTTG	GGGGAGTTG	CTTGCGACCG	TTGCTCGAA	GGGGCGTGTG	660
AAACCGTGTCA	ACGGGACCCCG	AAAGCTGACC	GGGTGACCGG	ATCTGAAAT	TGACCGGCTTA	720
GAACGGGGCGG	TTGGTGGTTA	TTCTTCGCTG	CTTCGGGCTTG	CTGGGACGGG	GGGGAGGTGG	780
CGGTCTTTGA	CGCGCTGAGCT	CTGGCGTTTG	AGGGCGACGA	CTTCAGGATG	GGGGAGGAGG	840
CGGTGCGATCA	TGGCGGACCG	ACGGACCTCG	TCGGGGCGGA	AAACCTGAAAT	GGGGCGGCGG	900
AAACCGCTTAT	TGGACGTGAC	GTGCAASCTG	CGGCGCTGAT	ACGGGAGGAA	GGGGAGCTCG	960
AAACGAGAGCT	TGGGGCGCTC	GGGTCAAC	GGATGTCAC	CGACTTCGTC	AAACGACCGG	1020
ACGGGAGATG	GGGGAGACCC	CTGGGTTTCG	GGGTGCGATG	GGGGCGCTG	GGGGAGGCTCG	1080
GGGAGACCGT	CTACCCATTC	GGGGCGCTG	GGGAGACGA	GGGGATGACG	GGGGCGACAC	1140
GGGGCGCTCG	GGGGCGCTG	GGGAGACGA	GGGGATGACG	GGGGCGACAC	GGGGCGACAC	1200
GGGGCGCTCG	GGGGCGCTG	GGGAGACGA	GGGGATGACG	GGGGCGACAC	GGGGCGACAC	1260
TTTGGGGCGA	GGGGCGCTG	GGGAGATGAT	GGGGCGCTG	GGGGCGACAC	GGGGCGACAC	1320
GGGGCGCGGG	ATGGGGCGCT	GGGGCGCTG	GGGGCGACAC	GGGGCGACAC	GGGGCGACAC	1380
GGGGCGCGGG	GGGGCGCTG	GGGGCGCTG	GGGGCGACAC	GGGGCGACAC	GGGGCGACAC	1440
GGGGCGCGGG	GGGGCGCTG	GGGGCGCTG	GGGGCGACAC	GGGGCGACAC	GGGGCGACAC	1482

(2) INFORMATION FOR SEQ ID NO:19:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCCGCA CGACCCCGCC ATAGCTTCTG GCGCCUCGCGC GACCGATGCG CTCGAGGGTT	60
CGTCCTCCGG CGCACCGCGCG CGCGGACCCAC CCTGACCGGT GAGGGCCCTGC AACACGGCGA	120
CGGTACGTG TTGCTGCTGG AGCGACCGAA CGCGGGGGTG GTTCGCTACG ACCGGGCTT	180
CGCGTACGAA ATCGGCTACA TCGGGAAAG CGCGCTGGCG AGGATGCGCG CGAGAGAACCC	240
CGACGACATC TTCTTCTACA TCACCGCTCA CGACCGGTG TACGTGCGAU CGCGGAGCC	300
CGCGACATTC ATCGGCGCG CGCGCGCTGGG CGCTATCTACG CGCGGACCGA	360
CGACCGCGAC AGACGACGCG AGATGCTGGC CTCCGGGATA CGGATGCGCG CGCGGCTGG	420
CGCGACGACAG ATGCTGCGCG CGCGCGTGGG TCGCGCGCGC GAGGTGCGT CGTGTGCG	480
TTGGGGCGAG CTAAACCGCG ACACGGGTGGT CATCGAGACC CGAGACGCG CGCGACCGCG	540
TCGGGGCGCG CGCGGTGGCGT AGCTGCGAG AGCGTGGCG ATGCTGCG CGCGGTGAT	600
CGCGGTGCGT GACTGCGATCG CGCGCGTGGC CGACGACATC CGACCGCTGG CGCGGGCGAC	660
ATGCTGCGAC TTGGGGCGAG AGCGGTGGCG TTTTTGCGCGAC ACTCGGGCGCG CGCGGTGGCG	720
TTGACTGCGAC ACCGACCGCG ACATGCGCGT CGTGTGCGCGT TTTGGGGCGAG CGTGGGGCGCG	780
CGACGCGCGTCA ATATGCGCG CGTGGCGCGAC CGCGGGCGCG CGCGGGCGCG AGTACCGCG	840
ATTCGCGCGAA CGTGGGGCGAG CGCGGGCGCG AGTACCGCG	876

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCGGGGGCGT CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	60
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CGAGATTCATA	ACGAAATTAC	ACGCGCACAA	CATATATGCG	CGATCGCGGT	TTATTTTGAC	120
ACCCGAGACC	TCCCACCGTT	CCCGAAGCAT	TTTACAGGCC	AAACCGCTGA	CCACCGAACG	130
CATGCCATGA	TCTCTCTGCA	ACACCTGCTC	GGCGCGACG	TTCCGCTGCGA	AATTCCCGGC	240
GTAGACACCG	TCGAAAGCA	TTTCCACAGA	CCCTCGAGG	CACTGCGCTT	GGCGCTCGAT	300
CACCAACCA	CACTGCGCA	CCAGCTGCT	CCCTGACAG	CCCTGCGCT	CCACCGAGCC	360
GATTTCTCG	GGCGACCGTT	CACTGCTCG	TTCTTGTGCG	AAACAGATGA	AGACGCTGCG	420
TTGATGCGCA	CCCTGGTCCG	GGTTGCGAT	CGCGCGGGG	CCAACTGTT	CGAGCTAGAG	480
AACTTCCTCG	CACTGAACT	GGATGTTGGG	CGCGCGCAT	CGCGCGCCC	CCACCGCTGCC	540
GGGGCGGGCG	TCTAGATCG	TCGGGGCAT	CACTGCTCG	TCCTGTTGCG	CCCGCGCTGT	600
TCCAGGCCAG	CCPTGCTCG	CCCGCGCTCG	TCAGTACCGA	TCAGACCGAC	CCCGACGCTCG	660
CCGAAAGCT	CAATGCTCTC	GTACTCTCG	ACCTTGCAGG	AGTACACCCG	CCGGCGCTGA	720
GCTGCCGAGC	GGTCAACGAG	TTGGGGATAT	TCCTTTACG	CAAGCACTGA	CGCTCCGACG	780
GGGGTTGGCG	CAACGGCCGT	GGCGGACTG	CTGCTGAGT	ATCGGGGGGT	CTTGGCGAAC	840
AAACAACCTG	CAAGGACCGG	TCGAGCGGGC	CGATACCGA	GGCGGGCGAG	CCGAAACCGA	900
CATGACCGCC	CGACGGGATC	GAATGCGGA	CGCGCTCG	CGATACCGA	ACGGGTGTAG	960
CGCGCGACG	AGTTGTTTTT	CCACCAAGA	ACCGTTTGC	GGTCATCGG	GGCAGTTAACG	1020
T						1021

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGGCCGCG	AACCGGACAA	CGACGGCATG	AGATGTTGGA	AATGGATGCG	CGAGGCTCTG	60
ACCGGCGGGG	CTGGCATCGG	CCCGCGCTCG	CCCGCTGCGA	CTTCGATCTG	GGCTGGCGGN	120
CCGGCTGCTAT	ACCAAGATGA	CCCGCTGCTC	TTGGGGGGCG	CACTGCGCTT	CCACCGCGNA	180

TCGGCCGCTG AAGCTCCGAC CCACCGCCAG TGACAGAGAC TGCTCAACAG AGTCGAGCGAT	240
CCACACGTGT CCTTTCGAA CAAAGGAACT CTGCTCGAGC GAGGAAATGG AGGAAAGGAG	300
GGGGAGGATC GAGGAGCACA A	321

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATGCTT TCCGGTTGCC GCGCGTTTTT CGCGCGCGAT CCTTAACCGC CTCGGCCAGC	60
CGATCCACCG CGCGCGAGAC CTGCGCTCG ATTACTCGCG CGCGCTGGAG CTCCCGGGGC	120
CTCGCTGCTT GAAACGCGAA GCGCGGAAAG AGCGCTTGA GACCGGGATC AGGGCGATTG	180
ACCGGATGAC CGCGATGGC CGCGCGCC CGCACGCTGAT CATCGGGAC CGCAAGACCG	240
GCAAAACCG CCTCTCTGTG CGACACCAT CCTCAACCG CGCGGAGAA CTGGGAGTCC	300
GCTGGATCCC AAGAAGGAGG TCCGGTTGTC TATACGTTGC CGATCGGGCA AGGAGGGGAA	360
CTTACCATCG CGG	373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGCGCGGCTT CGCGGGATTC CTGGCGGGGG CGCGCGCGCTT CGCGCTGGTG GATCGCGAC	60
TGGTTCACCG CGTGGGGCAA CGCTCGCTGT TTGCTCAAGGC AGCGCGCTGTC CGCTGCTGT	120
TCTTGACGGC CTGCTACGGG TTGGCGGATT TACCGGAGAT CGAGGGGGC GATCGGGTC	180
TGATCGATCTT CGTACCGCC CGTGGGGAA TGCGCGCTTG CGACGCTGCT CGCGCGTGG	240

GGCTGCGGT TTTCGTCGCC GCGAGCGTC GAGATGGGA CACGCTCCSC GCGATTCGCT	360
TTGACCCACCA AGCATATCGG AGATTCCCGC AGATTCGAA TTCCGAAAGCA GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCGGCG TTCATTCGGT TCCACCGGGG GCGCGGATA ATGGACGAGC TGTGAGGCC	60
GGCGTTGGG GCGCTCATGG CTGACAGCGA GATATGCA AGTTCTCTCG TATATGCCAC	120
CTACGCTTCA GTTGCTTGGG AGATGCTTT CTACGCTCA TGGATGTCAC CGTTTCGGT	180
GGCGACGCT CATGCTGGG GCGTACATCC TGGCGAGGG TGTGGCGGT CTGGGGCTCG	240
GCGCGCGTC CGCAGCCCGA ACCGCGCGG TGGCGACTA CTACTGTCG CGCGGGCAGC	300
CTTTGCGGCC CGCATGGGG AGTGGTACAC GTCGCGTCAC GAGTTCCGCC	360
GGGAGAGCA CGGCGCGAGC CACAGCGGGG AGTGGCGGG ACCGATGTCG GAGGTCCCG	420
TCTTGCAGCA TCGGGCTCT CGCGCGCGC CGCGCGCTAC CGGTGCGCGT CGATAGCGCT	480
CGTTGACGG CGCGCATGCA CGATACGGG TATGAGCGG AGCGTCCCGT CGCGAGCTA	540
CGACCGCGCG CGGGGCGAGT TTACGCTCCG CTGGCGATG AGTGGCGGGT CGATGACAG	600
AAATATGCGG AGCGTTTTCG CAAGCGCTG GAGCGCTT GAGGGAGCG TGTGATGAGC	660
CGCGACGCCG CCTCCACCAT CGACATGAC AGCGTTTTA CGCGACGCCG CGTTGCGCG	720
ATCGTG	726

(2) INFORMATION FOR SEQ ID NO:25:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGCGACGG AGGAGGCTCG CGGCGACCGAC CGCGCTATCGCG TTGATCGCGCG CGACCGGGAT	60
CGTGTGGCGAC CATACTCGAG CGTGTGGCGT CGCGCTGAG CGACGTTTG AGCGACGGCG	120
CTGCGCGATG CGGGCGCGGT GAACTCATCG CGCGCGCGCT TGTCCACCTG ATGAAACCGA	180
ATAGGCGACA ATAGGCGCGT GATTTGGCGAG TTGATGTCGCG CGTATGCCCG GAAATCCGAT	240
CGCGCGCGAT CGTCGGCGCC GACCGGGCTC CGCGCGCGCG CGCGCGCGA ATCTGGAGCG	300
AGCGATCGAT CGCGCGCGTG AAGCGCGCGA CGCGCGCGCG TCGTTTGCGAA GCGACTTACG	360
AGCGCGCGCG CATTGTGATG CGACTACCGAC TTGAGCGCTCG CGGTGGCGCTC CGCGCGAGCG	420
TGACACCGAA CGAACCGCGC CGACTGGCTG AGCGATCGAA AGCGCTTACT AGCTAACGCC	480
AGCGCGCGCG CGAATGCCCG CGCGTACCGCG CGCGCGCTTCG CGTAGATGTC CGTGTCTGCC	540
TGCGCGATGT ATGCGCGACG GAACTCTTGC ATAGGCGCGT	580

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAAGGAGGCG CGGGGGGGTTT TGGGGGGGGCG CGCGCGCTCG CGCGCGACCG CGGGGGCGCGC	60
CGTACCGCGCG CGTTGTTGCG TGTGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	120
CGTGTCAACCG CGACGTCGCG CGCGACACCG CGCGCGATCG	160

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCCATA CGATCTGTAT CTACGCCAAC TTTCCTGACCA CGCTCGAGGC TTTCACGATC	60
CAACGGACAC CGCGCGGCGT GACCTCGGCC ATGGGGGGCC CGTTCGCGGA CGCGCGCTGCG	120
AGGGCGATGG GAATCGACAA CCTCGCGGTA ATTCTACCG GAATGGACCC CGTCGTCUGCT	180
GAACGCCAAC ATTCGGACCA CGCGACAC ACCTTCGGCT TCGCGCGGGG TGTCTCTTC	240
CGCTTACGAGC GCGACGATCA GACCGACCGCG CG	272

(2) INFORMATION FOR SEQ ID NO:28:

(1) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 317 base pairs
- (b) TYPE: nucleic acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGAGCGCGTC TTTCCTGGAC TATCTCGCCA CGCTGACCGCA CGCGCGCGTG CGCGCGCTGA	60
ACCGGATCGA CGAGCGCGAT CGCGCTGGCGC CGTTCTCGCCG CTACCTGGCC CGTATCGCCG	120
CGCAAGGACCT GAACTGGCC CGACGGGGC CGCTCTCGCG CGTCGACGGG CGCGACGATCC	180
CGTCGGATCT CGCTCTGTC CGACGGGTCT ATCTCTGACCA TCGCGCGCCC CGCTCTGCGC	240
CGATCTCGAC CGCGACGATC AGCGACGCGT CGAACGTCGCG CGTCGCTGAC ATTCGGCTTCG	300
CGCGCTGGTT CGCGCGGG	317

(2) INFORMATION FOR SEQ ID NO:29:

(1) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 182 base pairs
- (b) TYPE: nucleic acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGCTGGAG CTGTCGATGA ACACGCTTCG CGGACGCGCG CGCGCGACCA CGTCGGTGTG	60
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GCGCGCGCGG AGCGCGCGCG CGCTCGCGAG CAGCTGATG ACCCGCGCGG CCTCGCGCCAC	120
CGCTTCGCGGC CGCTGACGAA ACACCGCGAC ACCGTCGCGG CGCGCGCGG ACCGGCGCGT	180
GG	182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGGAG TTTCGTCAC AGCGCGCGCG CGCGAAAGTC TGCGCGCGCG CGACCGCGCT	60
CGCGCGTCAC GAGGCGAGA CGCGCGTCAC CGAGCTGCTG CGACTGCTCT ACCGGCGCGCA	120
GAGCTTGAGA TTTCGTCAC CGCGCGAGTC GTAGCGAAACG TTTCGCGCGT CGATCGCTCAT	180
GAGACTCGGC CGCTTGGCAT TGACCGATGG CGCTGCGCGG TGCGCGACGA TTTCGCGCGT	240
CGCTTGGCAT ACCGCGCGCT CGACCGCTTT CGCGCGGAA CGCTGCGCGT ATCGACAGCG	300
ACGTTTGG	308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGAGGA CGCTGCGCG TGCGCGATGG CGCTGCGCGCG CATTGAGGAC CGACGAGGTC	60
CGCGCGAGG TGCGCGCGCG CAAGCTGCTCA TACTGACGG CGCTGAGGCG CTCCCCCGCGAT	120
CGCACCGGGAC TATTCGCTGC TGCGCGCGCG CGCTAACAGGC CGCTAACAGAGA ATGTCGCGCGC	180
ACCGCGATGAG CGATCGACGAC TACCGCGATCA TGCGCGATCT CGCGCGCTCG CGCGCGCGCG	240
TGCGCGCGCG ATCGACGGGC CGCTGCTCG	267

(2) INFORMATION FOR SSO ID NO:32:

4.1. SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x4) PROQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGCCTTA AACGATGTTCA GCGGACACCA TCGGCAATCA CCGCTACGCA GTCGTGAGA 60
TCTTCGGGAC CTGGCCCCAC CGCTCTCAGG CCGCAATCCA CGGGCGTTCG CGCGGAGCTG 120
CGCAAGGAT CGCGCGGCTG GACTGTTTG AAGTACGTC AATTCGAGGC CGCTGGTGG 180
ACGGAGCT CGCGCGGTTG CAGCTGACTA TGAAGTCGG CTTCGGCTGG AGCGTTCTG 240
AACCTTCAG CGCGGGGAT AACTGAGGTC CAGCTTAAG CGACGTTTCC AGAACATCCT 300
GACCGGTTG AACCGGGTT CGCGGAGGG TCGCTGGCC GAGGCGTTCG CTGGGAAATC 360
CCTGGGAGCA TTGCTGGGGCG CGCGCTACAA CGAAGCTGGT CGTCAATTGG TCGGGTATCT 420
GTCGACCTG TGTGGGGTGC AGCGGGACCA AGCGCTGTC CGCTGGAGT CGCGCTGGG 480
CGGGATGGCG TTGGCGGCTCA CGCGCTATCT GAGCGGCGAG CGAGGCTACG CGCGCTTGG 540
TATCTGGCG AACGGCGATCG CGTGGTCCCA CGCGGAGATC AGCTGGCGGC AGCGGAGCTT 600
CGAGTTCCAG CTCTGGAGCA TCTACAACTC CGTGTACAAAC CGAGAGGGA AATACGGTC 660
ACTAGACCTT CGCTTCCAT ATCGGGATCC CGCTGGAGT CGCGCTTTC TTACCTGGT 720
GTTCACCCAC ATGTTTCCCG CGAGCTGGA CGACTATCTG GAGCGGATCT CGCGGCTGGT 780
GAAGGCGGGCG CGACGATGCC TGTGGAGTA CTTCGGCTC ATGCGGAGT CGTGGGCCA 840
CATGGGCGAA CGAGAGACTG CGCACGACCT CGCGGAGAC CGCGGAGCTT ATCGGGACAT 900
CGCGGAGAA CGGGCGGGAG AACGAATGG CGTGGCGAG ACCTGGCTCA CGCGGCTCTA 960
TGGCAAGTTC CGCTTGGGGCG TCCACGAAAC ATTCGACCTAC CGCTGGTGA CGCGGGGGGAA 1020
ACGACGGCTA AGCTGGAGG AGCTGGTCAAT CGCGGAGAAA AGCGGAGCT AGGTGGGGAT 1080
CGGGGAGGCA TCGGGGAGCC CGAGGGCGCA CGCGGAGCTGC CGCGGAGGGCG ATTACGGGG 1140
CAGATTACCC CGCGGCGGGCT CGCGGCTGG AGTACGGCGC CGCGGATTCG CTGACGGGCT 1200
CGTAAAGGCG CTTCGGGGGGCG TCGGGGGCG CGCTGGAGT CGCTGGTGA ATGGCGGCGA 1260

AGCTTGCCTG	ATCGCTTCATC	ACCAACGGTC	ACAGGAGGCG	CTTGTGCGACCC	AGGGCCGACG	1320
CCACCCCCCT	CTCGGGGTCT	CTTCAGCGCGA	TCTGCGCGCC	CAAGCCGACACA	TGACCGAAACC	1380
CCGGCATCAC	CTTGCCTGATC	CCGCTTACCGT	GATACTTCTG	ATGTAATTTT	AACTGGCACCA	1440
ATAGATTTCG	ATCGGGCGAGA	ACTTGCCTGTC	CTTGCCTGCT	CAAGGCGCTG	ACCAAGCTGCC	1500
GGGGCGAAGA	CGGTATGGCG	TCTATCTTCG	CTCGCTGGCG			1539

(2) INFORMATION FOR SEQ ID NO:13:

III. SCIENCE CHARACTERISTICS

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[REDACTED] SEQUENCE DESCRIPTION: SEQ ID NO: 23;

CTCGACGGTC AGCTGGATCA GCGTCACCCC AGCGCGGGCC CGCGCTGACCG CGCGCGGAGCT 60
 CGCGCGTTCT CGCGCGGGCT ACCAGACCCC CTAGGGGCTC ACCGCTCCCT CGCGCGTGT
 CGCGCGAAC CGTGTGAAAC TGATGATTCT GATAGCGACC AACCTCTTGG CGCGCGAACAC 120
 CGCGCGGATC CGCGCTCAAG AGCGCGAATA CGCGCGATG TCGCGCGAAG ACCGCGCGCG 180
 GATGTTTGGC TACCGCGGGG CGCGCGGAC CGCGCGGGG ACCTTGTGCG CGTTCGAGGA 240
 CGCGCGGGAG ATGACCGCGG CGCGCTGGCT CGCGCGAAC CGCGCGGGG TCGCGCGAAC 300
 CTCGACGGAC CGCGCGGGCA ACCGCTTGAT GATGATGTC CGCGCGGGG TGAACAGTT 360
 CGCGCGGGCC ACCGCGGGCA CGCGCGGTC TTGCGAGCTG CGCGCGGGT CGAAGAGGT 420
 CTCGCGGGAT CGCTCGGGCA CGCGCGGAT CGCTCGGAT CGCGCGGGT CGAAGAGGT 480
 CGCGCGGGAT CGCTCGGGCA CGCGCGGAT CGCTCGGAT CGCGCGGGT CGAAGAGGT 540
 CGCGCGGGAT CGCTCGGGCA CGCGCGGAT CGCTCGGAT CGCGCGGGT CGAAGAGGT 600
 CGCGCGGGCC CGCGCGGGCG CGCGCGACCG CGCGCGGGG CGCGCGGGG CGATGAGGTC 660
 CGCGCGGGAC CGCGCGGGT CGCGCGGAT CGCGCGGGT CGCGCGGGG ACTTGGCG 720
 CGCGCGGGCTCG CGACGCTATG CGCACCGGA TCGCGGAA TATCGANAGT CGCGCGGGCG 780
 GAAACGCGTCT CGCGCGTAAG GTTACCGGGC GTTTCGCGGA TCGCGTAAAC TTGCGCGGG 840
 GAAACGCGTCT 851

(2) INFORMATION FOR SEQ ID NO:34:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATGATCGG	GGGGAAATT	TTT	GGACCGAGTT	CCGCTCCGGG	GATACCCAA	TCATCGAAC	60
CTAGATTTAT	TCCTTCTGAG	GGCGGAGTA	ATGGCTCGCA	GGAGACGAAAC	CTTACTGCTG		120
CGGGACGCG	TCGTTAGCTCC	TCGATACCGCC	GGGAGCCGTC	GCAATTTCG	ACGGACACGCC		180
CCATCGAAC	CTTCGAGGGC	CGCTCCGCT	TCTTGCGAG	GGCGGAGCT	CGCGCGCTGC		240
CGTTGCTCAA	CGTC						254

(2) INFORMATION FOR SEQ ID NO:35:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACG	GAAGGGGGCG	CCGCCAACGCG	GAATGCTG	TTCGACCGAG	ACCGACGGGA	60
CGATCTGGCG	CTGGCGATCG	CGGTTGAGTC	GGGGGGGTC	GCTGGATTCG	GCTATAACCT	120
TTCCTTCGAC	GAACGGGAGC	TCGATGCTGA	CCAAACCGCC	GATTCGCTG	GTGTCAGGTT	180
GATCGTGGAC	CGCGATGAGCG	CGCGCTATCT	GAAGGCGCC	TCATCGATT	TGTTGACACAC	240
TATTCGAGAC	CAAGTTTCAC	CATGGACAT	CCGACGCGA	CGCGCTGCTG	CGCGTGGCG	300
GATGTTTCA	ACTGATAAAA	CGCTGAGTACG	ACCGCGCGGT	CGCGACGCG	TACGACGACA	360
CGAAGGCTG	ACCGCTTGCG	AAAGACGACG	CGCGATGCC	TTGCGACGTA	CGCGCTGCG	420
GGCGGGCGCG	GGCGGGGTC	ACCTTCATCG	TCGACGACAC	CTGGCGCTGA	TATTCGACCC	480
ACGTCACGAT	TTTCAGGATG	GGCTGACATT	CGACGCGCA	CGATCGTTA	CGCGACCGGT	540

CCCTCTGAG CTTGGCCAAG GCGTGTGCGG ACCGCTTTCG CCGCACCGCC TGGTGATAC	630
CCGACAGCCC ATTGGGAAACG ATGGTTTCA CTTGGGTTT CTCGAGGCGG TTGAGGTATC	660
CTGTGATGCC GCTTTGGCC GTCGGTGGG AGAAATGTGGT TGGCGTTTTC GCTGGGTTGG	720
TGGGACCCC GATATGATC GCGGGGTCA TACCGAACAC CAGCGCGGGG GCTACACAA	780
TCCGATGAG CAGCGCTTC TACCGTGGT TCCGGTAAAG CAGCTGGGGG GCGACGGCG	840
GATATCCGG GCGGGGACG GCGCGCTCT CGGGGGGTGC CGGGGGGAGG GCGGGTTGG	900
GGGGGGGAG GTCGGGGGGG TACCGACGG CTTGGGTTTC GTCGGATGAG GCTGGGTT	960
AGGGGGGGGG TGGGTTGGT GCGACGGGG CGTTGGGGGG GTCGGGACGG GCGGGTGG	1020
TTCTCTTAAAG GTGGGGGACG GCGACGGGGT GTCGGGGGGG AACGGGGGGT GCGGGTGG	1080
GCGACGGGG GCAATGAGG TGGCTGGTCA GCGGGGGGGG GCGAAGGGGT GCGGGTGG	1140
CTCAACGGGA CGGGGGGGGG CGGGGGGGGG ATAAATGTTA AGGGGGGGGG AACGGTGGG	1200
ACGAACGGGG GAGATTTGGT GAGGAGTC	1227

(2) INFORMATION FOR SEQ ID NO:36:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGCTGGGGG CGGATGGGGG GCGGGTGGTCA AGGGGGGGGG GGGGGGGGGGG 63	
GGGGGGGGGG TACGGGGGGT GCGGGGGGGG AGGGGGGGT GTTGGGGGGGG GCGGGGGGG	120
GGGGGGGGGG GCGGGGGGGG GCGGGGGGGG GCGGGGGGGGG ATTTGGTGGT GCGGGGGGG	180
G	181

(2) INFORMATION FOR SEQ ID NO:37:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGTTTCCG CCGATCCGGC GGTGCTTGA ACCGCAACGG CGGTCTCGGC GGGGGGGGCG	60
GGGACGGCT TTTCGGCGGT GGGGGGGGCG AGGGCGGCT CGTGGCCAG GGGGGGATTA	120
GGGGGGGTC CACGGGGCGC AACGGGGTC TTGGGGGGCG CGGGGGTGGC GGAGGGAAAC	180
CTGGGGACGG CGGTTTGGT GGGAAACGGG CTAAGGGTGG CGGGGGCGG ATGGGGGGCG	240
GGGTCAAGAG CGGGACGGGGC CTGGGGGGTC AACGGGGTGA CGGGGGTGAC	300

(2) INFORMATION FOR SEQ ID NO:38:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCAGTGG CAGGGGGCT GTCAAGTGGAA GGT	34
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(2) INFORMATION FOR SEQ ID NO:39:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATGGCTCT CGTCCCCCGGC TTGGGGGGCGA CGGGGGGGCT CGGACGGTTA CGGACACAGG	60
TGGGGGGTC AGGACGGTC CGGGGGGGCG CGGGGGGGCG CGGGACGATG GGGACGGCTCG	120
TATGGGGACCG ATGGGGGGCG CGGGGGGGCG CGGG	135

(2) INFORMATION FOR SEQ ID NO:40:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGCCGTTCA CGGGGGGGGGG GGGACCGGGC ACCGGGGGGG GGGGGGGGGG TGG 53

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACGGC GGGTGCAGAC GGTGGGGGGG GGGGGACGGG GGGGGGGGGG GGGGGGGGG 66

GGACCGGGGGG CAACGGGGGG AACGGACGGG TGGTGGGGGG GGGGGGGGGG GGGGGGGGG 120

AGGGGGGGGGG CA 132

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCCGGGGC GGGAGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGG 66

CCGGCCGAGA ATGCTCCGAG TGGCGGCGATG GGGACGGGG GGGGGGGGGG GGGGGGGGG 120

GGGGGGGGGG CA 132

(2) INFORMATION FOR SEQ ID NO:43:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGGCGGCGGG	ATCGGTACCC	CGCGCGATCG	GGAGCTGGCC	ATTCGGGGGG	TTTCCCCCCC	60
CGACGGAAAC	CGCTTACCGA	TGGCGCTGCC	GAATGAGGCC	GTCCCGTTCC	CGATCCCCGC	120
ATGAGCGGC	GGCATGAAAT	TAGTGAGGA	ACCTTTGAGT	TTAGCCACCA	TAATGGCTAT	180
ACGCGTAAAG	AGGATGATCC	GTATTAACGC	ACTTCCAGAC	GGTGACCGTC	GTGAGGAG	240
ACATTGTTGA	CGGGCGGAC	GAATGGAGG	CTTGTGAGC	GGACCCACCG	ACTGATGTC	300
CCATCGACCC	GTGGGAACTC	ACCGGGGATA	AAAACCGGCC	CCACACGTC	GTNTTGTCCC	360
CCGCGACAT	GGGGGGATAC	CTGGGGGGCG	CTGGCGAAGA	GGGGCGGCGT	CTGGGGGACCT	420
CGCTGGAA	GGCGGCCAAG	GGTATGCCG	ACCTTGTG	CGACCGTCCG	ACCGCGCTCG	480
ACGAGACG	CGAAGGAACT	CTGCAGGCG	ATTCGGTTC	CGCGCTGCG	CGCGACGTT	540
CGGCGACAT	ACCGGATCC	CGAGGGTCC	CGACCGCTCG	TAACCGAAC	TTCATGGATC	600
TCAGAGACG	CGCGGGGAG	CTCGAAACCG	GGCGCCAG	GGCATGGCTC	GGCGCTGCG	660
GGGATGCGT	GAACACTTTC	ACCGTACCGC	TCGAAGGCGA	CG		720

(2) INFORMATION FOR SEQ ID NO:44:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAACCGGCG	CGCTGTCCC	CGGGTGGCG	CTGAAAGCG	CATGGCTCC	TGGCGTGG	60
GGCGGGGG	TGCGCTGCC	CGCTTCCGA	TCCCGGATCG	GGGGCGCGA	ATCGCTGCC	120
CGCGCTGCC	CTGGTACAT	TCGCGGTTA	CGCCCGGAA	GGGGCGCGG	CGCGCGCG	180

CTGGCCCGCG	CTGGCATGGG	AATGCCATG	GTGCCCCG	ATCAGGGACA	AAGGGGCGCC	240
AACTCCGAGG	TTTCTCAGCA	GGAGGAGGAG	GGCTCTTACA	CCGAGGATCC	TCTGCGCG	286

(2) INFORMATION FOR SEQ ID NO:45:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGCCACAGG	ATCGAATCCC	CTGGCCCGCA	CGCAGGCGTC	GCACTCACCC	ATGGAGGAG	60
CCATGACCTA	CTCGCGCGGT	AACCGCGGAT	ACCGCGACCC	CGAGCCCGCA	GGCTCTTACG	120
GAGGCGCTAC	ACCCCTCTTC	CCCGACGGCG	ATGAGGCTGC	GAGCAAGCTA	CCGATGTACG	180
TGAACATCGC	GGTGGCACTG	CTCGGTCTGG	CTGGCGCTTT	CGCCGCTTC	GGCCCGATGT	240
TCACCGCTCG	TACCGAAGTC	GGGGGGGCG	ATGGCGCGAT	CTCCGGCTAC	ATGCGGCTGC	300
CGCTCGCGAT	GGCTCTGCTG	CTGCGCTGTC	TTGGCGCGAT	GGTTCTGCTG	OCTAAGGCGA	360
AGACCCATGT	GACCTCTT	CGCGTCTCG	GGTACTCG	GGTATTCTCG	ATGCTCTCGG	420
CGACGTTAA	CAAGCCCCAGC	GGTATTGGA	GGTTTGGCG	ATTGTTGGGT	GTGTTGGCTT	480
TCATCTGTT	CAAGGGCGTT	GGGGGATCC	GGGGGTTTT	GGGGAGAGCC	GGGGTATCA	540
CGCGCGCG	GGCGCGCG	AAGTTCGACC	GGTATCGAC	GTACGGCGCG	TACGGCGACT	600
AGGGACATTA	CGGGTGGCGA	GGGGGGGGT	ATACAGCTCA	GGGGGGTGGT	CGGGAGGCGG	660
CGGGACTCGA	GTGGGGGGCG	GGGGCGACT	CTGGCGACCC	TCGGCGATAT	GGGTGGCGAT	720
ACGGCGCGTA	TTGGCGCGAT	GGGGCGAT	GGGGCGATCG	ATACAGCTCT	CAAGGGCGCG	780
CGCGCGCGCC	GGGGCGACTG	GGTGGCAAC	ATGGCGATCA	GGGGCGATCC	ACGGCGCGTA	840
CGGGCTTTCG	GGGGTTCAGCG	GGGGCGAC	GGGGCGATCG	GGGGCGCGCG	GGGGCGCGAT	900
GTGGGGCTCG	ATGCAACTAT	TCAGACCGCA	GGGGGGGCGA	GGGGCGCTCG	TCGGGGGGGG	960
GGGGCGCGAT	CTAACGGGGCG	GGGGCGCGAT	GGGGCGCGCG	GTGGGGCGCG	AGGGTCAACA	1020
GGGTGTGCGC	AGGGCGGGGAC	GGGGCGCGAT	GGGGCGCGCG	GGGGCGCGCG	AGGGTCAACA	1080

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGCGA GACCGATGCC CCTACCTCTG CGCAGGCCCG AGCTATTTC GACCGATCT	60
CGGGGACCT GAAAACCCAG ATCAGGACAG TGGAGTCAGC CGCAGGTTCC TTGCGGGGCC	120
AGTACGACCG CGCGCGCG AGCGCGCG AGCGCGCGCT CGTACGCTTC GAGGAGCG	180
CGATTAACCA GAGGAGCGA CTGGACGAGA TGTGCGCGA TATTCGTCAG CGCGCGCTCC	240
AATACTCGAG CGCGGAGGAGC GAGCGACAGC AGCGCGCTTC CGCGGAAATG CGCTTTCAC	300
CGCGTAATAC GAAAGAAC CGAACAA	327

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTGCGCAT GATGGCGTTG TCGACGCTGA CGGATTCTGT AGCGCGCTCG TTGGCATCAA	60
CCAACAAACCT GTTGGCGTGC CGAAATGTCG CGAACCGCTG GATUTCGGTC ATCPTTTCT	120
TCTTGTCTCG GAACTGCACA CGCGCGCGCT CGCGCTCGGAG TACGTTTCGG	170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCCCCCC CACCCCCCGT CCCCCCGGAA CGACCGCTCG CCGTGGGGGC AACGGGGGGG 60
CGGGGGTGG CGGGGGGAGC GATGGTTTCG TCTTCGGCAA CGGGGGTCCC CGGGGGGAGC 120
GGGGCT 127

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGGGGGAA CGGGGGACCC CGGGGGGGG CGGGGGGGG CGGGGGGGCA AACGGGGGAA 60
CGGGGGTCC CGGGGGAAACG C 81

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCACGGCT CGGGGGGGCT CGGGGGGAGA CGGGGGAAACG AGGGGGGGCC CGGGGGGGTC 60
CGAAACGGGGCG CGGGGGGGCT CGGGGGGGCT CGAAACGGGGCG CGGGGGGGCC CGGGGGGGCG 120
GAAACGGGGCG TCGGGGGCG CTGGATGGCG 149

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGGAGA TCACMCTAC CGACTGATCG AGATCGTGGCG GACCTCGGCC GACGGTGTGG	60
ACGGGAAAT CGAGGGCGT CTGGGCGGAG CTGGCGGAGAC CATGGCGCGCG CTGGGACTGGT	120
TGGAAGTACA GTCATTTGGA GGGACCTGGC TCGACGGAGC GGTGGGGGAC TTCCAGGTGA	180
CTATGAACT CGGGTTGGCG CTGGGGGATT CCTGAACTT CAAGGGGGGC CGTAACTGA	240
CGTGGTGTAT TAAGGGACTT TTCCAGGACA TCGTGGCGC CTGGAAACAC GGTTCAGGCC	300
ACGGTGGCTC CGGGAGGGG CGGGTCCAA ATGGGCGCG AGAATTGTC GGGCG	360

(z) INFORMATION FOR SEQ ID NO:52:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGGATCACC ATCACCACTA CGTCATCG AGTGGACCGG AGTTGACACG TGGCAAGGGA	60
CGATTGGCG CACTGGCTAT CGGGGGGATG CGGGGGGGCA CGCTGGTGAC CGTGGCGCG	120
CGGGGGGGCG CGAACGGGCG CGGGGGGGCG TGGGGGGGGG TACCCACACG CGGGGGGCG	180
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	240
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	300
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	360
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	420
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	480
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	540
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	600
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	660

GGCAACGGGG	TGTCTGGAG	GGCGGCGAT	TACCGACTCA	AGTTCAACCA	TCCGAGTAA	720
CCGACCGAAC	AGATCTGGAC	GGCGGCGATC	GGCTCGGGCG	GGCGGACGCC	ACGGGACGCC	730
GGCGGCGCTC	AGCGCTCGCT	TGGCTGATCG	CTCGCGGCGG	CCACGACGCC	GTGGACACAG	840
GGCGGCGCA	AGCGCTGGC	CGAATCGATC	GGCGGCTTGG	TGGCGCGCG	GGCGGCGCG	850
GGACCGGCTC	CTGAGAGCC	CGCTCGGGCG	GGCGGCGCG	CGGCGACGAT	CGCTCGTACG	960
GGGAGGACAC	CGACACCGCA	GGCGACCTTA	GGGGCGCTGA			999

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met	His	His	His	His	His	Met	His	Gln	Val	Asp	Pro	Asn	Leu	Thr	
1						10									15
Arg	Arg	Lys	Gly	Arg	Leu	Ala	Ala	Leu	Ala	Ile	Ala	Ala	Met	Ala	Ser
				20				25					30		
Ala	Ser	Leu	Val	Thr	Val	Ala	Val	Pro	Ala	Thr	Ala	Asn	Ala	Asp	Pro
				35				40				45			
Cys	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr
				50				55				60			
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro
				65				70				75			80
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala
				85				90				95			
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro
				100				105				110			
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly	Phe	Ser
				115				120				125			
Phe	Ala	Ile	Pro	Ala	Gly	Trp	Val	Gly	Ser	Asp	Ala	Ala	His	Phe	Asp
				130				135				140			
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro	Phe	Pro

145	150	155	160
Gly	Gln	Pro	Pro
Pro	Pro	Val	Ala
Asn	Asp	Thr	Arg
165	170	175	180
Leu	Asp	Gln	Lys
Lys	Leu	Tyr	Ala
Ser	Ala	Glu	Ala
Ala	Thr	Asp	Ser
185	190	195	200
Ala	Ala	Arg	Leu
Gly	Ser	Asp	Gly
Asp	Met	Gly	Glu
195	200	205	210
Phe	Tyr	Met	Pro
Tyr	Pro	Tyr	Phe
205	210	215	220
Gly	Thr	Arg	Ile
Thr	Asn	Asn	Gln
Val	Glu	Glu	Thr
Ser	Val	Val	Asp
210	215	220	225
Ser	Gly	Ser	Asp
Asp	Ser	Tyr	Tyr
225	230	235	240
Gly	Val	lys	Phe
230	235	240	245
Pro	Asn	Gly	Gln
Asn	Gln	Ile	Trp
245	250	255	260
Thr	Thr	Thr	Val
250	255	260	265
Ala	Asp	Ala	Gly
Asp	Pro	Pro	Gln
260	265	270	275
Arg	Arg	Trp	Phe
Trp	Val	Val	Val
270	275	280	285
Leu	Gly	Ala	Asn
275	280	285	290
Thr	Ala	Asn	Asn
Ala	Asn	Pro	Val
Asp	lys	Gly	Ala
285	290	295	300
Ala	Ala	Ala	lys
Asn	Asn	Asn	Ala
290	295	300	305
Pro	Ile	Arg	Pro
Asp	Asn	Asp	Leu
305	310	315	320
Pro	Pro	Pro	Val
Asn	Asn	Asn	Ala
310	315	320	325
Ala	Pro	Ala	Asp
Asn	Ala	Pro	Asn
315	320	325	330
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
320	325	330	335
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
325	330	335	340
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
330	335	340	345
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
335	340	345	350
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
340	345	350	355
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
345	350	355	360
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
350	355	360	365
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
355	360	365	370
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
360	365	370	375
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
365	370	375	380
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
370	375	380	385
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
375	380	385	390
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
380	385	390	395
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
385	390	395	400
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
390	395	400	405
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
395	400	405	410
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
400	405	410	415
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
405	410	415	420
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
410	415	420	425
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
415	420	425	430
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
420	425	430	435
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
425	430	435	440
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
430	435	440	445
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
435	440	445	450
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
440	445	450	455
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
445	450	455	460
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
450	455	460	465
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
455	460	465	470
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
460	465	470	475
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
465	470	475	480
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
470	475	480	485
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
475	480	485	490
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
480	485	490	495
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
485	490	495	500
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
490	495	500	505
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
495	500	505	510
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
500	505	510	515
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
505	510	515	520
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
510	515	520	525
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
515	520	525	530
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
520	525	530	535
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
525	530	535	540
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
530	535	540	545
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
535	540	545	550
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
540	545	550	555
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
545	550	555	560
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
550	555	560	565
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
555	560	565	570
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
560	565	570	575
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
565	570	575	580
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
570	575	580	585
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
575	580	585	590
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
580	585	590	595
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
585	590	595	600
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
590	595	600	605
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
595	600	605	610
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
600	605	610	615
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
605	610	615	620
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
610	615	620	625
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
615	620	625	630
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
620	625	630	635
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
625	630	635	640
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
630	635	640	645
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
635	640	645	650
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
640	645	650	655
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
645	650	655	660
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
650	655	660	665
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
655	660	665	670
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
660	665	670	675
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
665	670	675	680
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
670	675	680	685
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
675	680	685	690
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
680	685	690	695
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
685	690	695	700
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
690	695	700	705
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
695	700	705	710
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
700	705	710	715
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
705	710	715	720
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
710	715	720	725
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
715	720	725	730
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
720	725	730	735
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
725	730	735	740
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
730	735	740	745
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
735	740	745	750
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
740	745	750	755
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
745	750	755	760
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
750	755	760	765
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
755	760	765	770
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
760	765	770	775
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
765	770	775	780
Pro	Ala	Ala	Asn
Asn	Ala	Ala	Asn
770	775	780	785
Ala	Pro	Ala	Asn
Asn	Ala	Ala	Asn
775	780	785	790
Pro	Ala	Ala	Asn

(2) INFORMATION FOR SEQ ID NO:55:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Ieu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1														15

(2) INFORMATION FOR SEQ ID NO:56:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Iys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Ieu	Glu	Ala	Ala	Iys
1															15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1														15

(2) INFORMATION FOR SEQ ID NO:58:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Asn Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Cln Cln Thr Ser
1 5 10 15
Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Cys Gly Asp Arg Ser Gly Gly Asn Leu Asp Gln Ile Arg Leu Arg
1 5 10 15
Arg Asp Arg Ser Gly Gly Asn Leu
20

(2) INFORMATION FOR SDO ID NO: 64:

(ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Thr Gly Ser Leu Asn Glu Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Ile Thr Ala
 20 25 30
 Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45
 Gly Gly Pro Val Val Tyr Glu Met Glu Pro Val Val Phe Gly Ala Pro
 50 55 60
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Glu
 65 70 75 80
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85 90 95
 Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Ala Ala Arg
 100 105 110
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115 120 125
 Leu Ser Phe Ser Val Thr Asp Ile Glu Pro Ala Ala Ala Gly Ser Ala
 130 135 140
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145 150 155 160
 Glu Asn Val Thr Phe Val Asn Glu Gly Gly Trp Met Leu Ser Arg Ala
 165 170 175
 Ser Ala Met Glu Leu Leu Glu Ala Ala Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO: 65:

(ii) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Asp	Glu	Val	Thr	Val	Glu	Thr	Thr	Ser	Val	Phe	Arg	Ala	Asp	Phe	Leu
1					3					10					18
Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser															
					20				28					30	
Gly Val Gln Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg															
					35			40					45		
Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Thr Thr Ser															
					50			55				60			
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val															
					65			70				75			80
Ser Arg Arg His Ala Glu Phe Arg Leu Gln Asn Asn Gln Phe Asn Val															
					85			90				95			
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val															
					100			105				110			
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu															
					115			120				125			
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Gln Asp Asp Gly Ser															
					130			135				140			
Thr Gly Gly Pro															
					145										

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr	Ser	Asn	Arg	Pro	Ala	Arg	Arg	Gly	Arg	Arg	Ala	Pro	Arg	Asp	Thr
1					3					10					18

100

Gly	Pro	Asp	Arg	Ser	Ala	Ser	Ileu	Ser	Ieu	Val	Arg	His	Arg	Arg	Gln
20															30
Gln	Arg	Asp	Ala	Ieu	Cys	Ieu	Ser	Ser	Thr	Gln	Ile	Ser	Arg	Gln	Ser
35															45
Asn	Ieu	Pro	Pro	Ala	Ala	Gly	Gly	Ala	Ala	Asn	Tyr	Ser	Arg	Arg	Asn
50															60
Phe	Asp	Val	Arg	Ile	Lys	Ile	Phe	Met	Ieu	Val	Thr	Ala	Val	Val	Ieu
65															80
Ieu	Cys	Cys	Ser	Gly	Val	Ala	Thr	Ala	Ala	Pro	Lys	Thr	Tyr	Cys	Glu
85															95
Glu	Ieu	Lys	Gly	Thr	Asp	Thr	Gly	Gln	Ala	Cys	Gln	Ile	Gln	Met	Ser
100															110
Asp	Pro	Ala	Tyr	Asn	Ile	Asn	Ile	Ser	Ieu	Pro	Ser	Tyr	Tyr	Pro	Asp
115															125
Gln	Lys	Ser	Ieu	Gln	Asn	Tyr	Ile	Ala	Gln	Thr	Arg	Asp	Lys	Phe	Ieu
130															140
Ser	Ala	Ala	Thr	Ser	Ser	Thr	Pro	Arg	Glu	Ala	Pro	Tyr	Glu	Ieu	Asn
145															160
Ile	Thr	Ser	Ala	Thr	Tyr	Gln	Ser	Ala	Ile	Pro	Pro	Arg	Gly	Thr	Gln
165															175
Ala	Val	Val	Ieu	Xaa	Val	Tyr	His	Asn	Ala	Gly	Gly	Thr	His	Pro	Thr
180															190
Thr	Thr	Tyr	Asn	Ala	Asp	Trp	Asp	Gln	Ala	Tyr	Arg	Lys	Pro	Ile	
195															205
Thr	Tyr	Asp	Thr	Ieu	Trp	Gln	Ala	Asp	Thr	Asp	Pro	Ieu	Pro	Val	Val
210															220
Phe	Pro	Ile	Val	Ala	Arg										
225															

(2) INFORMATION FOR SEQ ID NO:67:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

(2) INFORMATION FOR SEQ ID NO: 68:

(ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
 65 70 75 80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
 85 90 95

Ser Glu Arg Lys
 100

(2) INFORMATION FOR REQ ID NO: 69:

(a) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[xii] SEQUENCE DESCRIPTION: SEQ ID NO: 60

Met Thr Asp Asp Ile Ieu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr	1	5	10	15
Ieu Thr Ieu Asn Arg Pro Gln Ser Arg Asn Ala Ieu Ser His Ala Ieu	20	25	30	
Arg Asp Arg Phe Phe Ala Xaa Ieu Xaa Asp Ala Glu Xaa Asp Asp Asp	35	40	45	
Ile Asp Val Val Ile Ieu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly	50	55	60	
Ieu Asp Ieu Iys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Ieu	65	70	75	80
Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Glu Arg	85	90	95	
Arg Arg Gly Glu Arg Arg Ala Arg Thr Gly His Val Ieu Arg His Pro	100	105	110	
Asp Arg Leu Arg Ala Arg Pro Ieu Arg Arg His Pro Arg Pro Gly Gly	115	120	125	
Ala Ala Ala His Ieu Gly Thr Glu Cys Val Ieu Ala Ala Iys Gly Arg	130	135	140	
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg	145	150	155	160
Asp Arg Arg				

(2) INFORMATION FOR SEQ ID NO:10:

(ii) FREQUENCY CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Met	Lys	Phe	Val	Asn	Asn	Ile	Glu	Pro	Val	Ala	Pro	Arg	Arg	Ala	Gly
1															15
Gly	Ala	Val	Ala	Glu	Val	Tyr	Ala	Glu	Ala	Arg	Arg	Glu	Phe	Gly	Arg
															20
															25
															30
Leu	Pro	Glu	Pro	Ileu	Ala	Met	Leu	Ser	Pro	Asp	Glu	Gly	Leu	Leu	The
															35
															40
															45
Ala	Gly	Trp	Ala	Thr	Leu	Arg	Glu	Thr	Leu	Ileu	Val	Gly	Gln	Val	Pro
															50
															55
Arg	Gly	Arg	Lys	Glu	Ala	Val	Ala	Ala	Val	Ala	Ala	Ser	Leu	Arg	
															60
															65
Cys	Pro	Trp	Cys	Val	Asp	Ala	His	Thr	Thr	Met	Leu	Tyr	Ala	Ala	Gly
															70
															75
															80
Gln	Thr	Asp	Thr	Ala	Ala	Ile	Leu	Ala	Gly	Thr	Ala	Pro	Ala	Ala	
															100
															105
															110
Gly	Asp	Pro	Asn	Ala	Pro	Tyr	Val	Ala	Trp	Ala	Ala	Gly	Thr	Gly	The
															115
															120
															125
Pro	Ala	Gly	Pro	Pro	Ala	Pro	Phe	Gly	Pro	Asp	Val	Ala	Ala	Gly	Tyr
															130
															135
															140
Leu	Gly	Thr	Ala	Val	Gln	Phe	His	Phe	Ile	Ala	Arg	Leu	Val	Leu	Val
															145
															150
															155
															160
Leu	Leu	Asp	Glu	Thr	Phe	Leu	Pro	Gly	Gly	Pro	Arg	Ala	Gln	Gln	Leu
															165
															170
															175
Met	Arg	Arg	Ala	Gly	Gly	Ileu	Val	Phe	Ala	Arg	Arg	Val	Arg	Ala	Glu
															180
															185
															190
His	Arg	Pro	Gly	Arg	Ser	Thr	Arg	Arg	Ileu	Gly	Pro	Arg	Thr	Ileu	Pro
															195
															200
															205
Asp	Asp	Leu	Ala	Trp	Ala	The	Pro	Ser	Glu	Pro	Ile	Ala	Thr	Ala	The

210	215	220
Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro		
225	230	235
Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro		
245	250	255
Met Pro Met Ser Ser Arg Trp Thr Asn Gln His Thr Ala Glu Leu Pro		
260	265	270
Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Ile Thr Gly Leu Ala		
275	280	285
Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu		
290	295	300
Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr		
305	310	315
Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln		
320	325	330
Val Ser Arg Gln Asn Pro Thr Gly		
340		

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala		
1	5	10
Ile Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu		
20	25	30
Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile		
35	40	45
Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu		
50	55	60
Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu		
65	70	75
80		

105

Arg Glu Arg Tyr Leu Leu His Asp Glu Gin Gly Arg Pro Ala Glu Ser
 85 86 87 88

The Gly Gin Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Ala Glu
 100 101 102 103 104 105 106 107 108 109 110

Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
 115 116 117 118 119 120 121 122 123 124 125

Thr Leu Leu Arg Asn Leu Glu The Leu Pro Asn Ser Pro Thr Leu Met
 130 131 132 133 134 135 136 137 138 139 140

Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys The Val Leu Pro
 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160

Ile Gin Asp Ser Leu Gin Ser Ile Phe Ala Thr Leu Gly Glu Ala Ala
 165 166 167 168 169 170 171 172 173 174 175

Glu Leu Gin Arg Ala Gly Gly Gly The Gly Tyr Ala The Ser His Leu
 180 181 182 183 184 185 186 187 188 189 190

Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly The Ala Ser Gly
 195 196 197 198 199 200 201 202 203 204 205

Pro Val Ser The Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 211 212 213 214 215 216 217 218 219 220

Met Gly Gly Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240

His Pro Asp Ile Cys Asp The Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 246 247 248 249 250 251 252 253 254 255

Glu Leu Pro His Phe Asn Leu Ser Val Gly Val The Asp Ala Phe Leu
 260 261 262 263 264 265 266 267 268 269 270

Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 276 277 278 279 280 281 282 283

Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 285 286 287 288 289 290 291 292 293

Cys Iys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320

Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 326 327 328 329 330 331 332 333

The Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 341 342 343 344 345 346 347 348

Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 356 357 358 359 360 361 362 363

Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp

106

370	375	380
Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala		
385	390	395
Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu		
405	410	415
Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg		
420	425	430
Leu Ala Thr Arg Leu Met Arg Arg Ile Glu Glu Ala Ala His Thr Ala		
435	440	445
Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp		
450	455	460
Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Glu Val Thr Ser		
465	470	475
Val Ala Pro Thr Gly		
480		

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly Val Ile Val Ieu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Ala		
1	5	10
Ile Tyr Trp Arg Arg Arg Gly Leu Ala Ieu Gly Ile Ala Val Val Val		
	20	25
Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala		
35	40	45
Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Glu Ser His		
50	55	60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Glu Thr Glu		
65	70	75
Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Glu Asn Pro Glu Thr Pro		
85	90	95

Thr	Pro	Thr	Ala	Ala	Val	Gln	Pro	Pro	Pro	Val	Ieu	Lys	Glu	Gly	Asp
106							105					110			
Asp	Cys	Pro	Asp	Ser	Thr	Ieu	Ala	Val	Lys	Gly	Ieu	Thr	Asn	Ala	Pro
115						120						125			
Gln	Tyr	Tyr	Val	Gly	Asp	Gln	Pro	Lys	Phe	Thr	Met	Val	Val	Thr	Asn
130						135				140					
Ile	Gly	Ieu	Val	Ser	Cys	Lys	Arg	Asp	Val	Gly	Ala	Ala	Val	Ieu	Ala
145						150			155			160			
Ala	Tyr	Val	Tyr	Ser	Ieu	Asp	Asn	Lys	Arg	Ieu	Trp	Ser	Asn	Ieu	Asp
165						170						175			
Cys	Ala	Pro	Ser	Asn	Glu	Thr	Ieu	Val	Lys	Thr	Phe	Ser	Pro	Gly	Glu
180						185						190			
Gln	Val	Thr	Thr	Ala	Val	Thr	Trp	Thr	Gly	Met	Gly	Ser	Ala	Pro	Arg
195						200				205					
Cys	Pro	Ieu	Pro	Arg	Pro	Ala	Ile	Gly	Pro	Gly	Thr	Tyr	Asn	Ieu	Val
210						215					220				
Val	Gln	Ieu	Gly	Asn	Ieu	Arg	Ser	Ieu	Pro	Val	Pro	Phe	Ile	Ieu	Asn
225						230			235			240			
Gln	Pro	Pro	Pro	Pro	Gly	Pro	Val	Pro	Ala	Pro	Gly	Pro	Ala	Gln	
245						250						255			
Ala	Pro	Pro	Pro	Glu	Ser	Pro	Ala	Gln	Gly	Gly					
260						265									

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu	Ile	Ser	Thr	Gly	Lys	Ala	Ser	His	Ala	Ser	Ieu	Gly	Val	Gln	Val
1								10					15		
Thr	Asn	Asp	Lys	Asp	Thr	Pro	Gly	Ala	Lys	Ile	Val	Glu	Val	Val	Ala
20						25						30			
Gly	Gly	Ala	Ala	Ala	Asn	Ala	Gly	Val	Pro	Lys	Gly	Val	Val	Val	Thr
35						40						45			

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 56 58 60
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gin Asp
 65 70 75 80
 Pro Ser Gly Gly Ser Arg Thr Val Gin Val Thr Leu Gly Lys Ala Glu
 85 90 95
 Glu

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20 25 30
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50 55 60
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65 70 75 80
 Gly Val Thr Glu Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85 90 95
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
 100 105 110
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
 115 120 125
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
 130 135 140
 Thr Thr Ala Lys Ile Thr Asn Gly Thr Ile Thr Val Trp Asn Asp Pro

109

145	150	155	160
Ala Ile Gln Ala Ile Asn Ser Gly Thr Asp Ile Pro Pro Thr Pro Ile			
165	170	175	
Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln			
180	185	190	
Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser			
195	200	205	
Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly			
210	215	220	
Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Gln			
225	230	235	240
Trp Ser Phe Ala Val Gly Lys Gln Ile Asn Met Ala Gln Ile Ile Thr			
245	250	255	
Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys			
260	265	270	
Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu			
275	280	285	
Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile			
290	295	300	
Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr			
305	310	315	320
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly			
325	330	335	
Gin Gln Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe			
340	345	350	
Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser			
355	360		

(3) INFORMATION FOR SEQ ID NO:75:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

110

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
 1 5 10 15

Gln Thr His Glu Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30

Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45

Pro Arg Arg His Pro Ala Glu Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80

Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
 85 90 95

Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110

Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Glu Pro Asp Arg Asp
 115 120 125

Ala Asp His Gly Ala Pro Val Arg Gly Arg Pro His Arg Gly Val
 130 135 140

Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160

Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175

Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190

Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205

Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220

Ala Gly Pro Glu Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240

Leu Pro Ala Arg Ala Gly Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255

Arg Ala Gly Gly Ala Gln Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270

His Glu Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285

Ala Gly Val Ala His His Ala Ala Gly Pro Arg Arg Ala His Val Arg

III

290	295	300
Asn Arg Pro Arg Arg		
305		

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly		
1	5	10
		15

Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys		
20	25	30

Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala		
35	40	45

Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys		
50	55	60

Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr		
65	70	75
		80

Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser		
85	90	95

Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His		
100	105	110

Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Ile Val Gln		
115	120	125

Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro		
130	135	140

Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Glu Gln Thr		
145	150	155
		160

Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln		
165	170	175

Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro		
180	185	190

Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205

Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220

Ile Ala Val Val Ser Ala Gly Ile Gly Ala Ala Ala Ser Leu Val
 225 230 235 240

Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255

Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270

Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285

Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300

Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys
 305 310 315 320

Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
 325 330 335

Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp
 340 345 350

Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser
 355 360 365

Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile
 370 375 380

Gly Ser Pro Leu Gly Leu Gln Gly Thr Val Thr Thr Gly Ile Val Ser
 385 390 395 400

Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Gln Ala Gly Asn Gln Asn
 405 410 415

Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn
 420 425 430

Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn
 435 440 445

Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly
 450 455 460

Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile
 465 470 475 480

Ala Asp Gln Leu Ile Ser Thr Gly Lys Ala Ser Gln Ala Ser Leu Gly

485	490	495
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Gln		
500	505	510
Val Val Ala Gly Gly Ala Ala Asn Ala Gly Val Pro Lys Gly Val		
515	520	525
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Ieu		
530	535	540
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Ieu Thr		
545	550	555
Thr Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly		
560	570	575
Lys Ala Glu Gln		
580		

(i) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANGLINESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Ieu Val Val Ieu			
1	5	10	15
Gly Ala Cys Leu Ala Ieu Trp Ieu Ser Gly Cys Ser Ser Pro Lys Pro			
20	25	30	
Asp Ala Glu Glu Glu Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro			
35	40	45	
Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu			
50	55	60	
Thr Ser Val Gln Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Ieu			
65	70	75	80
Ieu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Ieu Ala			
85	90	95	
Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Glu Gln Gly Val Pro Phe Arg			
100	105	110	

114

Val	Gln	Gly	Asp	Asn	Ile	Ser	Val	Lys	Ieu	Phe	Asp	Asp	Trp	Ser	Asn	
113																
															123	
Leu	Gly	Ser	Ile	Ser	Ser	Glu	Leu	Ser	Thr	Ser	Arg	Val	Leu	Asp	Pro	Ala
130																140
Ala	Gly	Val	Thr	Gln	Leu	Leu	Ser	Gly	Val	Thr	Asn	Leu	Gln	Ala	Gln	
145																155
																165
Gly	Thr	Glu	Val	Ile	Asp	Gly	Ile	Ser	Thr	Thr	Lys	Ile	Thr	Gly	Thr	
165																175
Ile	Pro	Ala	Ser	Ser	Val	Lys	Met	Leu	Asp	Pro	Gly	Ala	Lys	Ser	Ala	
180																190
Arg	Pro	Ala	Thr	Val	Trp	Ile	Ala	Gln	Asp	Gly	Ser	His	His	Leu	Val	
195																205
Arg	Ala	Ser	Ile	Asp	Leu	Gly	Ser	Gly	Ser	Ile	Gln	Leu	Thr	Gln	Ser	
210																220
Lys	Trp	Asn	Gln	Pro	Val	Asn	Val	Asp								
225																230

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	Pro	Thr	Ser	Trp	Gln	Gln	Ala	Ala	
1																15
Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg	Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	
20																20
Ala	Arg	Val	Ile	Glu	Gln	Asp	Met	Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	
35																45
Thr	Tyr	Arg	Ile	Lys	Leu	Gln	Val	Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	
50																60
Pro	Arg															
65																

(2) INFORMATION FOR SEQ ID NO:79:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1 5 10 15

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
20 25 30

Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Ser
35 40 45

Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
50 55 60

Ser Pro Pro Ile Pro
65

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
1 5 10 15

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
20 25 30

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
35 40 45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
50 55 60

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
65 70 75 80

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Gln Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Ala Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

(2) INFORMATION FOR SEQ ID NO:81:

(d) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO: 81

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Gly	Asp	Ser	Thr	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Thr	Val	
1	5							10				15				
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Ieu	Thr	Gly	Glu	Gly	Leu	Gln	
	20							25				30				
His	Ala	Asp	Gly	His	Ser	Leu	Ieu	Ieu	Asp	Ala	Thr	Asn	Pro	Ala	Val	
	35							40				45				
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Gly	Ile	Gly	Tyr	Ile	Xaa	Glu	
	50							55				60				
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Gly	Asn	Pro	Gly	Asn	Ile	Phe	Phe	
	65							70				75			80	
Tyr	Ile	Thr	Val	Tyr	Asn	Gly	Pro	Tyr	Val	Gln	Pro	Pro	Gly	Pro	Glu	
	85							90				95				
Asn	Phe	Asp	Pro	Gly	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala	
	100							105				110				
Ala	Thr	Gly	Gln	Arg	Thr	Asn	Lys	Xaa	Gly	Ile	Ieu	Ala	Ser	Gly	Val	
	115							120				125				
Ala	Met	Pro	Ala	Ala	Ieu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Gly	Trp	
	130							135				140				
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Gly	Leu	Asn	
	145							150				155			160	
Arg	Asp	Gly	Val	Val	Ile	Gly	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg	
	165							170				175				
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Ieu	Gly	Asn	Ala	Arg	Gly	
	180							185				190				
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Gly	Gly	Ile	
	195							200				205				
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Leu	Gly	Thr	Asp	Gly	Ser	
	210							215				220				
Gly	Phe	Ser	Asp	Thr	Arg	Phe	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp	

225	230	235	240
Ala Glu Ser Gin Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg			
245	250	255	
Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Glu			
260	265	270	
Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Lys Lys			
275	280	285	

(2) INFORMATION FOR SRO ID NO: 831

(iii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr	Lys	Phe	His	Ala	Ieu	Met	Gln	Glu	Gln	Ile	Ala	Asp	Glu	Phe	Thr
1															15
Ala	Ala	Gln	Gln	Tyr	Val	Ala	Ile	Ala	Val	Tyr	Phe	Asp	Ser	Glu	Asp
				20						25					30
Ieu	Pro	Gln	Ieu	Ala	Lys	Phe	Tyr	Ser	Gln	Ala	Val	Clu	Glu	Arg	
					35			40							45
Asn	Ris	Ala	Met	Met	Ieu	Val	Gln	His	Ieu	Ieu	Asp	Arg	Asp	Ieu	Arg
					50			55							60
Val	Glu	Ile	Pro	Gly	Val	Asp	Thr	Val	Arg	Asn	Gln	Phe	Asp	Arg	Pro
					65			70				75			80
Arg	Glu	Ala	Ieu	Ris	Ieu	Ala	Ieu	Asp	Gln	Glu	Arg	Thr	Val	Thr	Asp
					85				90						95
Gln	Val	Gly	Arg	Ieu	Thr	Ala	Val	Ala	Arg	Asp	Glu	Gly	Asp	Phe	Ieu
					100				105						110
Gly	Glu	Gln	Phe	Met	Gln	Trp	Phe	Ieu	Gln	Glu	Gln	Ile	Gln	Gln	Val
					115			120							125
Ala	Ieu	Met	Ala	Thr	Ieu	Val	Arg	Val	Ala	Asp	Arg	Ala	Gly	Ala	Asn
					130			135							140
Ieu	Phe	Glu	Ieu	Glu	Asn	Phe	Val	Ala	Arg	Glu	Val	Asp	Val	Ala	Pro
					145			150				155			160

120

Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
 1 5 10 15

Ala Ala Gly Leu Thr Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
 20 25 30

Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
 35 40 45

Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
 50 55 60

Val Pro Thr Ala Ala Gln Trp Thr Xaa Ileu Leu Asn Xaa Leu Xaa Asp
 65 70 75 80

Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
 85 90 95

Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
 100 105

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
 1 5 10 15

Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr

121

20 25 30

Arg Arg Ala Leu Glu Leu Glu Ala Pro Ser Val Val Xaa Arg Glu Gly
 35 40 45

Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 50 55 60

Pro Ile Gly Arg Gly Glu Arg Glu Leu Ile Ile Gly Asp Arg Lys Thr
 65 70 75 80

Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu
 85 90 95

Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr
 100 105 110

Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg
 115 120 125

(2) INFORMATION FOR SEQ ID NO:86:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val
 1 5 10 15

Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala
 20 25 30

Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu
 35 40 45

Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala
 50 55 60

Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp
 65 70 75 80

Gly Val Glu Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu
 85 90 95

Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa
 100 105 110

Arg Ser Ser Asn Gly
115

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Ile
1 5 10 15

Ala Thr Gly Val Ala Gly Ile Gly Val Gly Ala Gln Ser Ala Ala Gln
20 25 30

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
35 40 45

Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
50 55 60

His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
65 70 75 80

Ile Leu Glu Gly Pro Val Ile Asp Asp Pro Gly Ala Ala Pro Pro Pro
85 90 95

Pro Ala Ala Gly Gly Gly Ala
100

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Val Glu Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
1 5 10 15

Ala	Asp	Gln	Ala	Arg	Ala	Gly	Gly	Pro	Ala	Arg	Ile	Trp	Arg	Glu	His
20									28					30	
Ser	Met	Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Gly	Ala
35						40						45			
Thr	Lys	Gly	Gly	Arg	Gly	Ile	Val	Met	Arg	Val	Pro	Leu	Glu	Gly	Gly
50						55					60				
Gly	Arg	Leu	Val	Val	Glu	Leu	Thr	Pro	Asp	Glu	Ala	Ala	Ala	Leu	Gly
65					70				75					80	
Asp	Glu	Leu	Lys	Gly	Val	Thr	Ser								
					85										

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Thr	Asp	Ala	Ala	Thr	Leu	Ala	Gln	Gln	Ala	Gly	Asn	Phe	Glu	Arg	Ile
1					5				10			15			
Ser	Gly	Asp	Leu	Lys	Thr	Gln	Ile	Asp	Gln	Val	Glu	Ser	Thr	Ala	Gly
					20			25			30				
Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala	Ala	Gly	Thr	Ala	Ala	Gln	Ala
					35			40			45				
Ala	Val	Val	Arg	Phe	Gln	Glu	Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu
					50			55			60				
Asp	Gln	Ile	Ser	Thr	Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg
					65			70			75			80	
Ala	Asp	Gln	Glu	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	The		
						85			90			95			

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Thr	Gln	Ser	Gln	Thr	Val	Thr	Val	Asp	Gln	Gln	Glu	Ile	Leu	Asn
1															15
Arg	Ala	Asn	Glu	Val	Glu	Ala	Pro	Met	Ala	Asp	Pro	Pro	Thr	Asp	Val
															30
Pro	Ile	Thr	Pro	Cys	Glu	Leu	Thr	Xaa	Xaa	Lys	Asn	Ala	Ala	Gln	
															45
Xaa	Val	Leu	Ser	Ala	Asp	Asn	Met	Arg	Glu	Tyr	Leu	Ala	Ala	Gly	Ala
															60
Lys	Glu	Arg	Gln	Arg	Leu	Ala	Thr	Ser	Leu	Arg	Asn	Ala	Ala	Lys	Xaa
															65
Tyr	Gly	Glu	Val	Asp	Glu	Glu	Ala	Ala	Thr	Ala	Leu	Asp	Asn	Asp	Gly
															85
Glu	Gly	Thr	Val	Gln	Ala	Glu	Ser	Ala	Gly	Ala	Val	Gly	Gly	Asp	Ser
															105
Ser	Ala	Glu	Leu	Thr	Asp	Thr	Pro	Arg	Val	Ala	Thr	Ala	Gly	Glu	Pro
															125
Asn	Phe	Met	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Lys	Leu	Glu	Thr	Gly	Asp
															140
Gln	Gly	Ala	Ser	Leu	Ala	His	Xaa	Gly	Asp	Gly	Trp	Asn	Thr	Xaa	Thr
															160
Leu	Thr	Leu	Gln	Gly	Asp										
															165

(2) INFORMATION FOR SEQ ID NO:91:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg	Ala	Glu	Arg	Met
1				6

(2) INFORMATION FOR SEQ ID NO: 92:

(iii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Val Ala Trp Met Ser Val Thr Ala Gly Gin Ala Glu Leu Thr Ala Ala
1 S 10 15

Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Ile Thr
20 25 30

Val Pro Pro Pro Val Thr Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35 40 45

Ile Ala The Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile His Val Asn
80 85 90

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gin Asp Ala Ala Ala Met Phe
65 70 75 80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85 90 95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Lys Ile Glu Glu Ala
100 105 110

Ala Ala Val Glu Glu Gln Ala Ser Asp Thr Ala Ala Ala Asp Glu Ileu Met
103 120 128

Asn Asn Val Pro Gin Ala Leu Iys Gin Leu Ala Gin Pro Thr Gin Gly
130 135 140

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Ilys Thr Val Ser Pro
145 150 155 160

Sis Arg Ser Pro Ile Ser Asn Met Val Ser Met Asp Ala Asn Asn His Met
165 170 175

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Lys Ser Ser Met
100 105 110

Leu Lys Glu Phe Ala Pro Ala Ala Ala Glu Ala Val Glu Thr Ala
195 200 205

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly

210	215	220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Ieu Gly Arg Ala Ala		
225	230	235
Ser Val Arg Tyr Gly Asn Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly		
245	250	255
Arg Arg Asn Gly Gly Pro Ala		
260		

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala		
1	5	10
15		
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly		
20	25	30
35		
Ala Ser Lys Ieu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly		
35	40	45
50		
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr		
50	55	60
65		
Gly Leu Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
65	70	75
80		
Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val		
85	90	95
100		
Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu		
100	105	110
115		
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr		
115	120	125
130		
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln		
130	135	140
145		
Ala Val Ala Ala Val Leu Ala Leu Val Gln Thr Gly Ala Ile Thr		
145	150	155
160		

Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg
 165 170 175
 Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly
 180 185 190
 Gln Gln Gly Ala Gln Gln Ala Gly Leu Gln Ser Pro Gly Pro Gln
 195 200 205
 Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser
 210 215 220
 Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala
 225 230 235 240
 Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser
 245 250 255
 Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser
 260 265 270
 Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn
 275 280 285
 Pro Ser Gly Gly Gln Gln Ser Ser Ser Pro Gly Gly Ala Pro Val
 290 295 300

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAAAGATGG TGAATTCAT CGCCCGAGCT CTGACCGCCG CGCTCTGAACT CGGCAGCCGCT 60
 CGGGCGGCTG TGACTTCAT CAGGGCTGC CGCGCGGCTG TTAACGAGAT CGACGGCGTC 120
 CTUTTCGGCG CGCGACTGCCG GTTGGACCGCG CGTCGCGCCG CTGAGCTGCCG GCGCGCGCGC 180
 CATTGACCA GGTGTTGAA CGCGCTGCCG CGTCCAAAGG TUTGCTTTCG GAGCAGGGCG 240
 ACTCTGCTCC AGGGCGGCT CGGGCGGCTG CGCGCGGCA TCGCGAACCA CGAGCTGAAG 300
 AAGGCGCGCG AGGACGGGGA TCTGGCGCGTC TGTTCAGCG CGCGAACAT CGAGCGCGCG 360
 CGCGCGCGTT CGACGCTGCCG CGACGTTTCG GTCTCGGGTC CGAGCTTTCG GTCGCGCGTC 420

ACCCAGACAGG	TCACCTTCGGT	CAATCAAGGC	GGCTGGATGC	TTCACGGCC	ATTCGGATG	480
GAGTTGGCTG						567

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala						
1	5	10	15			
Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro						
	20	25	30			
Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu						
	35	40	45			
Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Ileu Thr Ser						
	50	55	60			
Leu Leu Asn Ser Ile Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly						
	65	70	75	80		
Ser Leu Val Gln Gly Gly Ile Gly Thr Glu Ala Arg Ile Ala Asp						
	85	90	95			
His Lys Leu Lys Ilys Ala Ala Gln His Gly Asp Leu Pro Leu Ser Phe						
	100	105	110			
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp						
	115	120	125			
Val Ser Val Ser Gly Phe Ilys Leu Ser Ser Pro Val Thr Gln Asn Val						
	130	135	140			
Thr Phe Val Asn Gln Gly Gly Top Met Leu Ser Arg Ala Ser Ala Met						
	145	150	155	160		
Gln Leu Leu Gln Ala Ala Gly Asn						
	165					

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS: